

## SEQUENCE LISTING

<110> Merck & Co., Inc.

<120> POLYPEPTIDES FOR INDUCING A PROTECTIVE  
IMMUNE RESPONSE AGAINST STAPHYLOCOCCUS AUREUS

<130> 21569Y PCT

<150> 60/489,840

<151> 2003-07-24

<150> 60/520,115

<151> 2003-11-14

<160> 107

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 446

<212> PRT

<213> Artificial Sequence

<220>

<223> ORF0657n with amino terminus methionine

<400> 1

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Met Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr
 1             5             10             15
Glu Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu Thr
      20             25             30
Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala
      35             40             45
Pro Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala
      50             55             60
Pro Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn
      65             70             75             80
Thr Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro
      85             90             95
Ala Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp
      100            105            110
Phe Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala
      115            120            125
Ser Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu
      130            135            140
Ile Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val
      145            150            155            160
Tyr Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr
      165            170            175
Val Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys
      180            185            190
Ala Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys
      195            200            205

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Tyr Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala
 210                215                220
Asp Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala
225                230                235                240
Pro Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn
                245                250                255
Lys Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys
                260                265                270
Lys Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala
                275                280                285
Ile Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp
                290                295                300
Leu Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu
305                310                315                320
Ser Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu
                325                330                335
Asn Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp
                340                345                350
Lys Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp
                355                360                365
Ala Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys
                370                375                380
Thr Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr
385                390                395                400
Asp Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys
                405                410                415
Ala Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala
                420                425                430
Lys Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro
                435                440                445

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<210> 2  
 <211> 645  
 <212> PRT  
 <213> S. aureus

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<400> 2
Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys
 1                5                10                15
Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu Leu
                20                25                30
Met Ser Asn Gly Glu Ala Gln Ala Ala Glu Glu Thr Gly Gly Thr
                35                40                45
Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr
                50                55                60
Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser
65                70                75                80
Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala
                85                90                95
Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val Lys
                100                105                110
Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu
                115                120                125
Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser
                130                135                140

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Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe	Glu	Met	Lys	Lys	Lys	Asp	Gly
145					150					155					160
Thr	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser	Ser	Val	Lys	Pro	Ala	Arg	Val
				165					170					175	
Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile	Glu	Leu	Gly	Leu	Gln	Ser	Gly
			180					185					190		
Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr	Glu	Gly	Asp	Lys	Lys	Leu	Pro
		195					200					205			
Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val	Lys	Asp	Tyr	Ala	Tyr	Ile	Arg
	210					215					220				
Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	Val	Lys	Ile	Val	Ser	Ser	Thr
225					230					235					240
His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	Asp	Tyr	Thr	Leu	Met	Glu	Phe
				245	,				250					255	
Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	Lys	Phe	Lys	Thr	Glu	Glu	Asp
			260					265					270		
Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	Tyr	Lys	Lys	Ala	Lys	Thr	Leu
		275					280					285			
Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys	Ile	Gln	Asp	Lys	Leu	Pro	Glu
	290					295					300				
Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys	Leu	Glu	Asp	Thr	Lys	Lys	Ala
305					310					315					320
Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile	Thr	Glu	Phe	Gln	Asn	Val	Gln
				325					330					335	
Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu	Gln	Asp	Thr	Lys	Tyr	Val	Val
			340					345					350		
Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser	Met	Met	Asp	Thr	Phe	Val	Lys
		355					360					365			
His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	Gly	Lys	Lys	Tyr	Met	Val	Met
	370					375					380				
Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys	Asp	Phe	Met	Val	Glu	Gly	Gln
385				390						395					400
Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	Lys	Asn	Asn	Thr	Arg	Thr	Ile
				405					410					415	
Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr	Leu	Tyr	Asp	Ala	Ile	Val	Lys
			420					425					430		
Val	His	Val	Lys	Thr	Ile	Asp	Tyr	Asp	Gly	Gln	Tyr	His	Val	Arg	Ile
		435					440					445			
Val	Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala	Asn	Thr	Asp	Lys	Ser	Asn	Lys
	450					455					460				
Lys	Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys	Lys	Glu	Ala	Thr	Pro	Ala	Thr
465				470						475					480
Pro	Ser	Lys	Pro	Thr	Pro	Ser	Pro	Val	Glu	Lys	Glu	Ser	Gln	Lys	Gln
				485					490					495	
Asp	Ser	Gln	Lys	Asp	Asp	Asn	Lys	Gln	Leu	Pro	Ser	Val	Glu	Lys	Glu
			500					505					510		
Asn	Asp	Ala	Ser	Ser	Glu	Ser	Gly	Lys	Asp	Lys	Thr	Pro	Ala	Thr	Lys
	515						520					525			
Pro	Thr	Lys	Gly	Glu	Val	Glu	Ser	Ser	Ser	Thr	Thr	Pro	Thr	Lys	Val
	530					535					540				
Val	Ser	Thr	Thr	Gln	Asn	Val	Ala	Lys	Pro	Thr	Thr	Ala	Ser	Ser	Lys
545					550					555					560
Thr	Thr	Lys	Asp	Val	Val	Gln	Thr	Ser	Ala	Gly	Ser	Ser	Glu	Ala	Lys
				565					570					575	

Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn<sup>6</sup> Thr Asn Asp Gly  
                   580                  585                  590  
 His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys  
                   595                  600                  605  
 Ser Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu Pro  
                   610                  615                  620  
 Leu Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu Pro  
 625                  630                  635                  640  
 Arg Lys Arg Lys Asn  
                   645

<210> 3

<211> 569

<212> PRT

<213> Artificial Sequence

<220>

<223> ORF0657nH with amino terminus methionine

<400> 3

Met Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr  
 1                  5                  10                  15  
 Glu Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu Thr  
                   20                  25                  30  
 Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala  
                   35                  40                  45  
 Pro Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala  
                   50                  55                  60  
 Pro Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn  
 65                  70                  75                  80  
 Thr Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro  
                   85                  90                  95  
 Ala Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp  
                   100                  105                  110  
 Phe Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala  
                   115                  120                  125  
 Ser Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu  
                   130                  135                  140  
 Ile Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val  
 145                  150                  155                  160  
 Tyr Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr  
                   165                  170                  175  
 Val Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys  
                   180                  185                  190  
 Ala Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys  
                   195                  200                  205  
 Tyr Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala  
                   210                  215                  220  
 Asp Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala  
 225                  230                  235                  240  
 Pro Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn  
                   245                  250                  255  
 Lys Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys  
                   260                  265                  270

Lys Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala  
 275 280 285  
 Ile Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp  
 290 295 300  
 Leu Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu  
 305 310 315 320  
 Ser Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu  
 325 330 335  
 Asn Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp  
 340 345 350  
 Lys Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp  
 355 360 365  
 Ala Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys  
 370 375 380  
 Thr Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr  
 385 390 395 400  
 Asp Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys  
 405 410 415  
 Ala Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala  
 420 425 430  
 Lys Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro  
 435 440 445  
 Val Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys  
 450 455 460  
 Gln Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly  
 465 470 475 480  
 Lys Asp Lys Thr Pro Ala Thr Lys Pro Thr Lys Gly Glu Val Glu Ser  
 485 490 495  
 Ser Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala  
 500 505 510  
 Lys Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr  
 515 520 525  
 Ser Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala  
 530 535 540  
 Asn Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys  
 545 550 555 560  
 Asn Thr Gln Glu Asn Lys Ala Lys Ser  
 565

&lt;210&gt; 4

&lt;211&gt; 570

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH with amino terminus methionine-glycine

&lt;400&gt; 4

Met Gly Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys  
 1 5 10 15  
 Thr Glu Ala Val Ala Ser Pro Thr Thr Ser Glu Lys Ala Pro Glu  
 20 25 30  
 Thr Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu  
 35 40 45

Ala Pro Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys  
 50 55 60  
 Ala Pro Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn  
 65 70 75 80  
 Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn  
 85 90 95  
 Pro Ala Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile  
 100 105 110  
 Asp Phe Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr  
 115 120 125  
 Ala Ser Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro  
 130 135 140  
 Glu Ile Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu  
 145 150 155 160  
 Val Tyr Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp  
 165 170 175  
 Thr Val Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr  
 180 185 190  
 Lys Ala Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu  
 195 200 205  
 Lys Tyr Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser  
 210 215 220  
 Ala Asp Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu  
 225 230 235 240  
 Ala Pro Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu  
 245 250 255  
 Asn Lys Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys  
 260 265 270  
 Lys Lys Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser  
 275 280 285  
 Ala Ile Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr  
 290 295 300  
 Asp Leu Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn  
 305 310 315 320  
 Glu Ser Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met  
 325 330 335  
 Leu Asn Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr  
 340 345 350  
 Trp Lys Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys  
 355 360 365  
 Asp Ala Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly  
 370 375 380  
 Lys Thr Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp  
 385 390 395 400  
 Tyr Asp Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr  
 405 410 415  
 Lys Ala Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser  
 420 425 430  
 Ala Lys Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser  
 435 440 445  
 Pro Val Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn  
 450 455 460  
 Lys Gln Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser  
 465 470 475 480

```
<210> 5
<211> 447
<212> PRT
<213> Artificial Sequence
```

```
<220>
<223> ORF0657nH with amino terminus methionine-glycine
```

- 7 -

```

Asn Lys Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys
    260                      265                      270
Lys Lys Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser
    275                      280                      285
Ala Ile Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr
    290                      295                      300
Asp Leu Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn
305                      310                      315                      320
Glu Ser Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met
    325                      330                      335
Leu Asn Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr
    340                      345                      350
Trp Lys Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys
    355                      360                      365
Asp Ala Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly
    370                      375                      380
Lys Thr Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp
385                      390                      395                      400
Tyr Asp Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr
    405                      410                      415
Lys Ala Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser
    420                      425                      430
Ala Lys Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro
    435                      440                      445

```

&lt;210&gt; 6

&lt;211&gt; 576

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 6

```

Ala Glu Glu Thr Gly Val Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
  1                      5                      10                      15
Ala Val Ala Ser Pro Thr Thr Thr Thr Thr Glu Lys Ala Pro Glu Ala
    20                      25                      30
Lys Pro Val Ala Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys
    35                      40                      45
Glu Val Val Ala Pro Thr Thr Glu Thr Lys Glu Ala Lys Glu Val Lys
    50                      55                      60
Ala Val Lys Glu Val Lys Ala Pro Lys Glu Ala Lys Glu Glu Lys Pro
65                      70                      75                      80
Ala Ala Lys Ala Asp Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu
    85                      90                      95
Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser Ala
    100                      105                      110
Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Lys Asp Gly Thr
    115                      120                      125
Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys Pro Ala Arg Val Ile
    130                      135                      140
Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly Gln
145                      150                      155                      160

```



Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro Ile  
 165 170 175  
 Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr Ala Tyr Ile Arg Phe  
 180 185 190  
 Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile Val Ser Ser Thr His  
 195 200 205  
 Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu Phe Ala  
 210 215 220  
 Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp Tyr  
 225 230 235 240  
 Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu Glu  
 245 250 255  
 Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp Lys Leu Pro Glu Lys  
 260 265 270  
 Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Glu Thr Lys Lys Ala Leu  
 275 280 285  
 Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln Pro  
 290 295 300  
 Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Val Tyr  
 305 310 315 320  
 Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp Ala Phe Val Lys His  
 325 330 335  
 Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met Glu  
 340 345 350  
 Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln Arg  
 355 360 365  
 Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile Ile  
 370 375 380  
 Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys Val  
 385 390 395 400  
 His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile Val  
 405 410 415  
 Asp Lys Glu Ala Phe Thr Lys Ala Asn Ala Asp Lys Thr Asn Lys Lys  
 420 425 430  
 Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Thr Thr Pro Ala Met Pro  
 435 440 445  
 Ser Lys Pro Thr Thr Pro Pro Val Glu Lys Glu Ser Gln Lys Gln Asp  
 450 455 460  
 Ser Gln Lys Asp Asp Asn Lys Gln Ser Pro Ser Val Glu Lys Glu Asn  
 465 470 475 480  
 Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Met Pro Val Thr Lys Pro  
 485 490 495  
 Ala Lys Ala Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val Val  
 500 505 510  
 Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Glu Thr  
 515 520 525  
 Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys Asp  
 530 535 540  
 Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly His  
 545 550 555 560  
 Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys Ser  
 565 570 575

&lt;210&gt; 7

&lt;211&gt; 568

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 7

Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu  
 1 5 10 15  
 Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys  
 20 25 30  
 Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro  
 35 40 45  
 Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro  
 50 55 60  
 Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr  
 65 70 75 80  
 Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala  
 85 90 95  
 Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe  
 100 105 110  
 Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser  
 115 120 125  
 Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile  
 130 135 140  
 Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr  
 145 150 155 160  
 Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val  
 165 170 175  
 Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala  
 180 185 190  
 Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr  
 195 200 205  
 Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp  
 210 215 220  
 Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro  
 225 230 235 240  
 Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys  
 245 250 255  
 Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys  
 260 265 270  
 Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile  
 275 280 285  
 Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu  
 290 295 300  
 Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser  
 305 310 315 320  
 Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn  
 325 330 335  
 Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys  
 340 345 350  
 Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala  
 355 360 365  
 Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr  
 370 375 380

```

Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp
385                      390                      395                      400
Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala
                      405                      410                      415
Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys
                      420                      425                      430
Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val
                      435                      440                      445
Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln
                      450                      455                      460
Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys
465                      470                      475                      480
Gly Val Thr Leu Ala Thr Lys Pro Thr Lys Gly Glu Val Glu Ser Ser
                      485                      490                      495
Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys
                      500                      505                      510
Pro Thr Thr Gly Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser
                      515                      520                      525
Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn
                      530                      535                      540
Ile Lys His Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn
545                      550                      555                      560
Thr Gln Glu Asn Lys Ala Lys Ser
                      565

```

&lt;210&gt; 8

&lt;211&gt; 568

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 8

```

Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
1      5      10      15
Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys
20     25     30
Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro
35     40     45
Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro
50     55     60
Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr
65     70     75     80
Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala
85     90     95
Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe
100    105    110
Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser
115    120    125
Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile
130    135    140
Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr
145    150    155    160

```

Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val  
                                   165                                  170                                  175  
 Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala  
                                   180                                  185                                  190  
 Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr  
                                   195                                  200                                  205  
 Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp  
                                   210                                  215                                  220  
 Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro  
 225                                  230                                  235                                  240  
 Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys  
                                   245                                  250                                  255  
 Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys  
                                   260                                  265                                  270  
 Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile  
                                   275                                  280                                  285  
 Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu  
                                   290                                  295                                  300  
 Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser  
 305                                  310                                  315                                  320  
 Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn  
                                   325                                  330                                  335  
 Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys  
                                   340                                  345                                  350  
 Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala  
                                   355                                  360                                  365  
 Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr  
                                   370                                  375                                  380  
 Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp  
 385                                  390                                  395                                  400  
 Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala  
                                   405                                  410                                  415  
 Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys  
                                   420                                  425                                  430  
 Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val  
                                   435                                  440                                  445  
 Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln  
                                   450                                  455                                  460  
 Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys  
 465                                  470                                  475                                  480  
 Asp Lys Thr Pro Ala Thr Lys Pro Thr Lys Gly Glu Val Glu Ser Ser  
                                   485                                  490                                  495  
 Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys  
                                   500                                  505                                  510  
 Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser  
                                   515                                  520                                  525  
 Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn  
                                   530                                  535                                  540  
 Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn  
 545                                  550                                  555                                  560  
 Thr Gln Glu Asn Lys Ala Lys Ser  
                                   565

&lt;210&gt; 9

&lt;211&gt; 568

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 9

Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu  
 1 5 10 15  
 Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys  
 20 25 30  
 Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro  
 35 40 45  
 Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro  
 50 55 60  
 Lys Glu Thr Lys Ala Val Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr  
 65 70 75 80  
 Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala  
 85 90 95  
 Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe  
 100 105 110  
 Glu Met Lys Lys Glu Asn Gly Glu Gln Gln Phe Tyr His Tyr Ala Ser  
 115 120 125  
 Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile  
 130 135 140  
 Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr  
 145 150 155 160  
 Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val  
 165 170 175  
 Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala  
 180 185 190  
 Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr  
 195 200 205  
 Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp  
 210 215 220  
 Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro  
 225 230 235 240  
 Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys  
 245 250 255  
 Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys  
 260 265 270  
 Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile  
 275 280 285  
 Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu  
 290 295 300  
 Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser  
 305 310 315 320  
 Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn  
 325 330 335  
 Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys  
 340 345 350  
 Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala  
 355 360 365  
 Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr  
 370 375 380

Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp  
 385 390 395 400  
 Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala  
 405 410 415  
 Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys  
 420 425 430  
 Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val  
 435 440 445  
 Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln  
 450 455 460  
 Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys  
 465 470 475 480  
 Asp Lys Thr Pro Ala Thr Lys Pro Thr Lys Gly Glu Val Glu Ser Ser  
 485 490 495  
 Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys  
 500 505 510  
 Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser  
 515 520 525  
 Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn  
 530 535 540  
 Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn  
 545 550 555 560  
 Thr Gln Glu Asn Lys Ala Lys Ser  
 565

&lt;210&gt; 10

&lt;211&gt; 568

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 10

Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu  
 1 5 10 15  
 Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys  
 20 25 30  
 Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro  
 35 40 45  
 Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro  
 50 55 60  
 Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr  
 65 70 75 80  
 Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala  
 85 90 95  
 Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe  
 100 105 110  
 Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser  
 115 120 125  
 Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile  
 130 135 140  
 Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr  
 145 150 155 160

Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val  
 165 170 175  
 Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala  
 180 185 190  
 Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr  
 195 200 205  
 Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp  
 210 215 220  
 Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro  
 225 230 235 240  
 Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys  
 245 250 255  
 Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys  
 260 265 270  
 Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile  
 275 280 285  
 Thr Glu Phe Gln Lys Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu  
 290 295 300  
 Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser  
 305 310 315 320  
 Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn  
 325 330 335  
 Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys  
 340 345 350  
 Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala  
 355 360 365  
 Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr  
 370 375 380  
 Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp  
 385 390 395 400  
 Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala  
 405 410 415  
 Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys  
 420 425 430  
 Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val  
 435 440 445  
 Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln  
 450 455 460  
 Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys  
 465 470 475 480  
 Asp Lys Thr Pro Ala Thr Lys Pro Thr Lys Gly Glu Val Glu Ser Ser  
 485 490 495  
 Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys  
 500 505 510  
 Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser  
 515 520 525  
 Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn  
 530 535 540  
 Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn  
 545 550 555 560  
 Thr Gln Glu Asn Lys Ala Lys Ser  
 565

&lt;210&gt; 11

&lt;211&gt; 565

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 11

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Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
 1          5          10          15
Ala Val Ala Ser Pro Thr Thr Thr Thr Glu Lys Ala Pro Glu Ala Lys
          20          25          30
Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro
          35          40          45
Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Ala Pro Lys Glu Thr
          50          55          60
Lys Ala Val Lys Pro Ala Ala Lys Ala Asp Asn Asn Thr Tyr Pro Ile
65          70          75          80
Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp
          85          90          95
Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys
          100          105          110
Lys Glu Asn Gly Glu Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys
          115          120          125
Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly
          130          135          140
Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp
145          150          155          160
Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr
          165          170          175
Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile
          180          185          190
Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr
          195          200          205
Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys
          210          215          220
Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys
225          230          235          240
Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp
          245          250          255
Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Asp
          260          265          270
Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe
          275          280          285
Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr
          290          295          300
Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp
305          310          315          320
Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys
          325          330          335
Tyr Met Val Met Glu Thr Thr Asn Asp Tyr Trp Lys Asp Phe Met
          340          345          350
Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn
          355          360          365
Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp
          370          375          380

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Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr  
 385 390 395 400  
 His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp  
 405 410 415  
 Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala  
 420 425 430  
 Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu  
 435 440 445  
 Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser  
 450 455 460  
 Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr  
 465 470 475 480  
 Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser Ser Thr Thr  
 485 490 495  
 Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr  
 500 505 510  
 Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser Ala Ser Ser  
 515 520 525  
 Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn  
 530 535 540  
 Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu  
 545 550 555 560  
 Asn Lys Ala Lys Ser  
 565

&lt;210&gt; 12

&lt;211&gt; 566

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 12

Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu  
 1 5 10 15  
 Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys  
 20 25 30  
 Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro  
 35 40 45  
 Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro  
 50 55 60  
 Lys Glu Thr Lys Ala Val Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr  
 65 70 75 80  
 Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala  
 85 90 95  
 Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe  
 100 105 110  
 Glu Met Lys Lys Glu Asn Gly Glu Gln Gln Phe Tyr His Tyr Ala Ser  
 115 120 125  
 Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile  
 130 135 140  
 Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr  
 145 150 155 160

Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val  
 165 170 175  
 Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala  
 180 185 190  
 Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr  
 195 200 205  
 Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp  
 210 215 220  
 Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro  
 225 230 235 240  
 Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys  
 245 250 255  
 Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys  
 260 265 270  
 Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile  
 275 280 285  
 Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu  
 290 295 300  
 Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser  
 305 310 315 320  
 Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn  
 325 330 335  
 Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys  
 340 345 350  
 Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala  
 355 360 365  
 Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr  
 370 375 380  
 Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp  
 385 390 395 400  
 Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala  
 405 410 415  
 Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys  
 420 425 430  
 Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val  
 435 440 445  
 Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln  
 450 455 460  
 Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys  
 465 470 475 480  
 Asp Lys Thr Pro Ala Thr Lys Pro Thr Lys Gly Glu Val Glu Ser Ser  
 485 490 495  
 Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys Pro  
 500 505 510  
 Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly  
 515 520 525  
 Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys  
 530 535 540  
 Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln  
 545 550 555 560  
 Glu Asn Lys Ala Lys Ser  
 565

&lt;210&gt; 13

&lt;211&gt; 568

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 13

Ala	Glu	Glu	Thr	Gly	Gly	Thr	Asn	Thr	Glu	Ala	Gln	Pro	Lys	Thr	Glu
1				5					10					15	
Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Ser	Glu	Lys	Ala	Pro	Glu	Thr	Lys
		20						25					30		
Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Glu	Ala	Pro
		35					40					45			
Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Glu	Val	Lys	Ala	Pro
	50				55						60				
Lys	Glu	Thr	Lys	Glu	Val	Lys	Pro	Ala	Ala	Lys	Ala	Thr	Asn	Asn	Thr
65				70					75						80
Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala
			85					90					95		
Ile	Lys	Asp	Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe
		100						105					110		
Glu	Met	Lys	Lys	Lys	Asp	Gly	Thr	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser
	115					120						125			
Ser	Val	Lys	Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile
	130					135						140			
Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr
145				150					155						160
Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val
			165					170					175		
Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala
		180						185					190		
Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr
	195						200					205			
Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp
	210					215					220				
Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro
225				230					235						240
Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys
			245						250					255	
Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys
		260						265					270		
Leu	Glu	Asp	Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile
	275						280					285			
Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu
	290					295					300				
Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser
305				310					315						320
Met	Met	Asp	Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn
			325					330					335		
Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	Thr	Asn	Asp	Asp	Tyr	Trp	Lys	
		340					345					350			
Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala
	355					360					365				
Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr
	370					375					380				

Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp  
 385 390 395 400  
 Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala  
 405 410 415  
 Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys  
 420 425 430  
 Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val  
 435 440 445  
 Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln  
 450 455 460  
 Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys  
 465 470 475 480  
 Asp Lys Thr Pro Ala Thr Lys Pro Thr Lys Gly Lys Val Glu Ser Ser  
 485 490 495  
 Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys  
 500 505 510  
 Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser  
 515 520 525  
 Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn  
 530 535 540  
 Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn  
 545 550 555 560  
 Thr Gln Glu Asn Lys Ala Lys Ser  
 565

&lt;210&gt; 14

&lt;211&gt; 568

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 14

Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu  
 1 5 10 15  
 Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys  
 20 25 30  
 Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro  
 35 40 45  
 Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro  
 50 55 60  
 Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr  
 65 70 75 80  
 Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Glu  
 85 90 95  
 Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe  
 100 105 110  
 Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser  
 115 120 125  
 Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile  
 130 135 140  
 Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr  
 145 150 155 160

Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Ala	Ser	Tyr	Asp	Thr	Val
				165					170					175	
Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Ile	Ser	Asn	Gly	Thr	Lys	Ala
			180					185					190		
Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr
		195					200					205			
Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp
	210					215					220				
Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro
225					230					235					240
Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys
				245					250					255	
Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys
			260					265					270		
Leu	Glu	Asp	Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile
		275					280					285			
Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu
	290					295					300				
Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser
305					310					315					320
Met	Met	Asp	Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn
				325					330					335	
Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys
			340					345					350		
Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala
	355					360						365			
Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr
	370					375					380				
Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val	His	Val	Lys	Thr	Ile	Asp	Tyr	Asp
385					390					395					400
Gly	Gln	Tyr	His	Val	Arg	Ile	Val	Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala
			405						410					415	
Asn	Thr	Asp	Lys	Ser	Asn	Lys	Lys	Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys
			420					425					430		
Lys	Glu	Ala	Thr	Pro	Ala	Thr	Pro	Ser	Lys	Pro	Thr	Pro	Ser	Pro	Val
	435						440					445			
Glu	Lys	Glu	Ser	Gln	Lys	Gln	Asp	Ser	Gln	Lys	Asp	Asp	Asn	Lys	Gln
	450					455					460				
Leu	Pro	Ser	Val	Glu	Lys	Glu	Asn	Asp	Ala	Ser	Ser	Glu	Ser	Gly	Lys
465					470					475					480
Asp	Lys	Thr	Pro	Ala	Thr	Lys	Pro	Ala	Lys	Gly	Glu	Val	Glu	Ser	Ser
				485					490					495	
Ser	Thr	Thr	Pro	Thr	Lys	Val	Val	Ser	Thr	Thr	Gln	Asn	Val	Val	Lys
			500					505					510		
Pro	Thr	Thr	Ala	Ser	S										

<210> 15  
<211> 564

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 15

Ala	Glu	Glu	Thr	Gly	Gly	Thr	Asn	Thr	Glu	Ala	Gln	Pro	Lys	Thr	Glu
1				5					10					15	
Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Thr	Glu	Lys	Ala	Pro	Glu	Ala	Lys
			20					25					30		
Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Glu	Ala	Pro
			35				40					45			
Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Ala	Pro	Lys	Glu	Thr
	50				55						60				
Lys	Ala	Val	Lys	Pro	Ala	Lys	Ala	Asp	Asn	Asn	Thr	Tyr	Pro	Ile	
65				70					75					80	
Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala	Ile	Lys	Asp
				85					90					95	
Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe	Glu	Met	Lys
			100					105					110		
Lys	Glu	Asn	Gly	Glu	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser	Ser	Val	Lys
		115					120					125			
Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile	Glu	Leu	Gly
	130					135					140				
Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr	Glu	Gly	Asp
145				150					155					160	
Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val	Lys	Asp	Tyr
			165						170					175	
Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	Val	Lys	Ile
			180					185					190		
Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	Asp	Tyr	Thr
		195					200					205			
Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	Lys	Phe	Lys
	210					215					220				
Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	Tyr	Lys	Lys
225					230					235				240	
Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys	Ile	Gln	Asp
			245						250					255	
Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys	Leu	Glu	Asp
		260						265					270		
Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile	Thr	Glu	Phe
		275					280					285			
Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu	Gln	Asp	Thr
	290					295					300				
Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser	Met	Met	Asp
305					310					315				320	
Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	Gly	Lys	Lys
			325						330					335	
Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Tyr	Trp	Lys	Asp	Phe	Met	
			340					345				350			
Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	Lys	Asn	Asn
		355					360					365			
Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr	Leu	Tyr	Asp
	370					375					380				

Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr  
 385 390 395 400  
 His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp  
 405 410 415  
 Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala  
 420 425 430  
 Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu  
 435 440 445  
 Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser  
 450 455 460  
 Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr  
 465 470 475 480  
 Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser Ser Thr Thr  
 485 490 495  
 Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Ala  
 500 505 510  
 Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser Ala Ser Ser Ser  
 515 520 525  
 Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr  
 530 535 540  
 Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn  
 545 550 555 560  
 Lys Ala Lys Ser

&lt;210&gt; 16

&lt;211&gt; 565

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 16

Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu  
 1 5 10 15  
 Ala Val Ala Ser Pro Thr Thr Thr Thr Glu Lys Ala Pro Glu Ala Lys  
 20 25 30  
 Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro  
 35 40 45  
 Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Ala Pro Lys Glu Thr  
 50 55 60  
 Lys Ala Val Lys Pro Ala Ala Lys Ala Asp Asn Asn Thr Tyr Pro Ile  
 65 70 75 80  
 Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp  
 85 90 95  
 Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys  
 100 105 110  
 Lys Glu Asn Gly Glu Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys  
 115 120 125  
 Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly  
 130 135 140  
 Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp  
 145 150 155 160

Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr  
 165 170 175  
 Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile  
 180 185 190  
 Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr  
 195 200 205  
 Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys  
 210 215 220  
 Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys  
 225 230 235 240  
 Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp  
 245 250 255  
 Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Asp  
 260 265 270  
 Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe  
 275 280 285  
 Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr  
 290 295 300  
 Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp  
 305 310 315 320  
 Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys  
 325 330 335  
 Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met  
 340 345 350  
 Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn  
 355 360 365  
 Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp  
 370 375 380  
 Ala Ile Val Arg Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr  
 385 390 395 400  
 His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp  
 405 410 415  
 Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala  
 420 425 430  
 Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu  
 435 440 445  
 Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser  
 450 455 460  
 Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr  
 465 470 475 480  
 Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser Ser Thr Thr  
 485 490 495  
 Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr  
 500 505 510  
 Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser  
 515 520 525  
 Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn  
 530 535 540  
 Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu  
 545 550 555 560  
 Asn Lys Ala Lys Ser  
 565

&lt;210&gt; 17

&lt;211&gt; 568



&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 17

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Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
 1          5          10          15
Ala Leu Ala Ser Pro Thr Thr Thr Thr Glu Lys Ala Pro Glu Thr Lys
          20          25          30
Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro
          35          40          45
Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro
          50          55          60
Lys Glu Thr Lys Ala Val Lys Pro Ala Ala Lys Ala Asp Asn Asn Thr
65          70          75          80
Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala
          85          90          95
Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe
          100          105          110
Glu Met Lys Lys Glu Asn Gly Glu Gln Gln Phe Tyr His Tyr Ala Ser
          115          120          125
Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile
          130          135          140
Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr
145          150          155          160
Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val
          165          170          175
Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala
          180          185          190
Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr
          195          200          205
Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp
210          215          220
Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro
225          230          235          240
Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys
          245          250          255
Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys
          260          265          270
Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile
          275          280          285
Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu
          290          295          300
Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser
305          310          315          320
Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn
          325          330          335
Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys
          340          345          350
Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala
          355          360          365
Ile Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr
370          375          380

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Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp  
 385 390 395 400  
 Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala  
 405 410 415  
 Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys  
 420 425 430  
 Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val  
 435 440 445  
 Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln  
 450 455 460  
 Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys  
 465 470 475 480  
 Asp Lys Thr Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser  
 485 490 495  
 Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys  
 500 505 510  
 Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser  
 515 520 525  
 Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn  
 530 535 540  
 Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn  
 545 550 555 560  
 Thr Gln Glu Asn Lys Ala Lys Ser  
 565

&lt;210&gt; 18

&lt;211&gt; 565

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 18

Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu  
 1 5 10 15  
 Ala Val Ala Ser Pro Thr Thr Thr Thr Glu Lys Ala Pro Glu Ala Lys  
 20 25 30  
 Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro  
 35 40 45  
 Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Ala Pro Lys Glu Thr  
 50 55 60  
 Lys Ala Val Lys Pro Ala Ala Lys Ala Asp Asn Asn Thr Tyr Pro Ile  
 65 70 75 80  
 Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp  
 85 90 95  
 Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys  
 100 105 110  
 Lys Glu Asn Gly Glu Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys  
 115 120 125  
 Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly  
 130 135 140  
 Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp  
 145 150 155 160

Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr  
 165 170 175  
 Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile  
 180 185 190  
 Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr  
 195 200 205  
 Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys  
 210 215 220  
 Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys  
 225 230 235 240  
 Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp  
 245 250 255  
 Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Asp  
 260 265 270  
 Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe  
 275 280 285  
 Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr  
 290 295 300  
 Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp  
 305 310 315 320  
 Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys  
 325 330 335  
 Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met  
 340 345 350  
 Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn  
 355 360 365  
 Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp  
 370 375 380  
 Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr  
 385 390 395 400  
 His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp  
 405 410 415  
 Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala  
 420 425 430  
 Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu  
 435 440 445  
 Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Pro Leu Pro Ser  
 450 455 460  
 Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr  
 465 470 475 480  
 Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser Ser Thr Thr  
 485 490 495  
 Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr  
 500 505 510  
 Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser Ala Ser Ser  
 515 520 525  
 Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn  
 530 535 540  
 Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu  
 545 550 555 560  
 Asn Lys Ala Lys Ser  
 565

&lt;210&gt; 19

&lt;211&gt; 568

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 19

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Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
 1          5          10          15
Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys
          20          25          30
Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro
          35          40          45
Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro
 50          55          60
Lys Glu Thr Lys Ala Val Lys Pro Ala Thr Lys Ala Asp Asn Asn Thr
65          70          75          80
Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala
          85          90          95
Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe
          100          105          110
Glu Met Lys Lys Glu Asn Gly Glu Gln Gln Phe Tyr His Tyr Ala Ser
          115          120          125
Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile
          130          135          140
Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr
145          150          155          160
Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val
          165          170          175
Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala
          180          185          190
Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr
          195          200          205
Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp
          210          215          220
Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro
225          230          235          240
Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys
          245          250          255
Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys
          260          265          270
Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile
          275          280          285
Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu
          290          295          300
Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser
305          310          315          320
Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn
          325          330          335
Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys
          340          345          350
Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala
          355          360          365
Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr
          370          375          380

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Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp  
 385 390 395 400  
 Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala  
 405 410 415  
 Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys  
 420 425 430  
 Arg Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val  
 435 440 445  
 Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln  
 450 455 460  
 Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys  
 465 470 475 480  
 Asp Lys Thr Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser  
 485 490 495  
 Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys  
 500 505 510  
 Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser  
 515 520 525  
 Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn  
 530 535 540  
 Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn  
 545 550 555 560  
 Thr Gln Glu Asn Lys Ala Lys Ser  
 565

<210> 20  
 <211> 568  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> ORF0657nH

<400> 20  
 Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu  
 1 5 10 15  
 Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys  
 20 25 30  
 Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro  
 35 40 45  
 Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro  
 50 55 60  
 Lys Glu Thr Lys Ala Val Lys Pro Ala Thr Lys Ala Asp Asn Asn Thr  
 65 70 75 80  
 Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala  
 85 90 95  
 Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe  
 100 105 110  
 Glu Met Lys Lys Glu Asn Gly Glu Gln Gln Phe Tyr His Tyr Ala Ser  
 115 120 125  
 Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile  
 130 135 140  
 Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr  
 145 150 155 160

Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val  
 165 170 175  
 Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala  
 180 185 190  
 Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr  
 195 200 205  
 Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp  
 210 215 220  
 Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro  
 225 230 235 240  
 Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys  
 245 250 255  
 Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys  
 260 265 270  
 Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile  
 275 280 285  
 Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu  
 290 295 300  
 Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser  
 305 310 315 320  
 Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn  
 325 330 335  
 Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys  
 340 345 350  
 Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala  
 355 360 365  
 Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr  
 370 375 380  
 Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp  
 385 390 395 400  
 Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala  
 405 410 415  
 Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys  
 420 425 430  
 Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val  
 435 440 445  
 Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln  
 450 455 460  
 Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys  
 465 470 475 480  
 Asp Lys Thr Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser  
 485 490 495  
 Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys  
 500 505 510  
 Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser  
 515 520 525  
 Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn  
 530 535 540  
 Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn  
 545 550 555 560  
 Thr Gln Glu Asn Lys Ala Lys Ser  
 565

&lt;210&gt; 21

&lt;211&gt; 576

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 21

Ala	Glu	Glu	Thr	Gly	Val	Thr	Asn	Thr	Glu	Ala	Gln	Pro	Lys	Thr	Glu	1	5	10	15
Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Thr	Thr	Glu	Lys	Ala	Pro	Glu	Ala	20	25	30	
Lys	Pro	Val	Ala	Lys	Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	35	40	45	
Glu	Val	Val	Ala	Pro	Thr	Thr	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	50	55	60	
Ala	Val	Lys	Glu	Val	Lys	Ala	Pro	Lys	Glu	Ala	Lys	Glu	Glu	Lys	Pro	65	70	75	80
Ala	Ala	Lys	Ala	Asp	Asn	Asn	Thr	Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu	85	90	95	
Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala	Ile	Lys	Asp	Lys	Asp	His	Ser	Ala	100	105	110	
Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe	Glu	Met	Lys	Lys	Lys	Asp	Gly	Thr	115	120	125	
Gln	Gln	Phe	Tyr	His	Tyr	Ala	Gly	Ser	Val	Lys	Pro	Ala	Arg	Val	Ile	130	135	140	
Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile	Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln	145	150	155	160
Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr	Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	165	170	175	
Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val	Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	180	185	190	
Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	Val	Lys	Ile	Val	Ser	Ser	Thr	His	195	200	205	
Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	210	215	220	
Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	225	230	235	240
Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	245	250	255	
Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys	Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	260	265	270	
Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys	Leu	Glu	Glu	Thr	Lys	Lys	Ala	Leu	275	280	285	
Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile	Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	290	295	300	
Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu	Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	305	310	315	320
Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser	Met	Met	Asp	Thr	Phe	Val	Lys	His	325	330	335	
Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	340	345	350	
Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys	Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	355	360	365	
Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	370	375	380	

Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys Val  
 385 390 395 400  
 His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile Val  
 405 410 415  
 Asp Lys Glu Ala Phe Thr Lys Ala Asn Ala Asp Lys Thr Asn Lys Lys  
 420 425 430  
 Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Thr Thr Pro Ala Met Pro  
 435 440 445  
 Ser Lys Pro Thr Thr Pro Pro Val Glu Lys Glu Ser Gln Lys Gln Asp  
 450 455 460  
 Ser Gln Lys Asp Asp Asn Lys Gln Ser Pro Gly Val Glu Lys Glu Asn  
 465 470 475 480  
 Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Met Pro Val Thr Lys Pro  
 485 490 495  
 Ala Lys Ala Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val Val  
 500 505 510  
 Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Glu Thr  
 515 520 525  
 Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys Asp  
 530 535 540  
 Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly His  
 545 550 555 560  
 Thr Gln Ser Gln Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys Ser  
 565 570 575

&lt;210&gt; 22

&lt;211&gt; 576

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 22

Ala Glu Glu Thr Gly Val Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu  
 1 5 10 15  
 Ala Val Ala Ser Pro Thr Thr Thr Thr Thr Glu Lys Ala Pro Glu Ala  
 20 25 30  
 Lys Pro Val Ala Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys  
 35 40 45  
 Glu Val Val Ala Pro Thr Thr Glu Thr Lys Glu Ala Lys Glu Val Lys  
 50 55 60  
 Ala Val Lys Glu Val Lys Ala Pro Lys Glu Ala Lys Glu Glu Lys Pro  
 65 70 75 80  
 Ala Ala Lys Ala Asp Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu  
 85 90 95  
 Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser Ala  
 100 105 110  
 Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Lys Asp Gly Thr  
 115 120 125  
 Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys Pro Ala Arg Val Ile  
 130 135 140  
 Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly Gln  
 145 150 155 160



Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro Ile  
 165 170 175  
 Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr Ala Tyr Ile Arg Phe  
 180 185 190  
 Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile Val Ser Ser Thr His  
 195 200 205  
 Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu Phe Ala  
 210 215 220  
 Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp Tyr  
 225 230 235 240  
 Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu Glu  
 245 250 255  
 Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp Lys Leu Pro Glu Lys  
 260 265 270  
 Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Glu Thr Lys Lys Ala Leu  
 275 280 285  
 Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln Pro  
 290 295 300  
 Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Val Tyr  
 305 310 315 320  
 Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp Thr Phe Val Lys His  
 325 330 335  
 Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met Glu  
 340 345 350  
 Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln Arg  
 355 360 365  
 Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile Ile  
 370 375 380  
 Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys Val  
 385 390 395 400  
 His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile Val  
 405 410 415  
 Asp Lys Glu Ala Phe Thr Lys Ala Asn Ala Asp Lys Thr Asn Lys Lys  
 420 425 430  
 Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Thr Thr Pro Ala Met Pro  
 435 440 445  
 Ser Lys Pro Thr Thr Pro Pro Val Glu Lys Glu Ser Gln Lys Gln Asp  
 450 455 460  
 Ser Gln Lys Asp Asp Asn Lys Gln Ser Pro Ser Val Glu Lys Glu Asn  
 465 470 475 480  
 Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Met Pro Val Thr Lys Pro  
 485 490 495  
 Ala Lys Ala Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val Val  
 500 505 510  
 Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Glu Thr  
 515 520 525  
 Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys Asp  
 530 535 540  
 Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly His  
 545 550 555 560  
 Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys Ser  
 565 570 575

&lt;210&gt; 23

&lt;211&gt; 568

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 23

Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu  
 1 5 10 15  
 Ala Val Ala Ser Pro Ser Thr Thr Thr Glu Lys Ala Pro Glu Ala Lys  
 20 25 30  
 Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro  
 35 40 45  
 Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro  
 50 55 60  
 Lys Glu Thr Lys Glu Val Lys Pro Ala Thr Lys Ala Asp Asn Asn Thr  
 65 70 75 80  
 Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala  
 85 90 95  
 Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe  
 100 105 110  
 Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser  
 115 120 125  
 Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile  
 130 135 140  
 Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr  
 145 150 155 160  
 Glu Gly Asn Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val  
 165 170 175  
 Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala  
 180 185 190  
 Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr  
 195 200 205  
 Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Gly  
 210 215 220  
 Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ser Pro  
 225 230 235 240  
 Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys  
 245 250 255  
 Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys  
 260 265 270  
 Leu Glu Glu Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile  
 275 280 285  
 Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu  
 290 295 300  
 Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser  
 305 310 315 320  
 Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn  
 325 330 335  
 Gly Lys Lys Tyr Met Val Met Glu Thr Asn Asp Asp Tyr Trp Lys  
 340 345 350  
 Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala  
 355 360 365  
 Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr  
 370 375 380

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Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp
385                      390                      395                      400
Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala
                      405                      410                      415
Asn Ala Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys
                      420                      425                      430
Lys Glu Thr Thr Pro Ala Thr Pro Ser Lys Pro Thr Thr Pro Pro Val
                      435                      440                      445
Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln
                      450                      455                      460
Ser Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys
465                      470                      475                      480
Asp Lys Thr Pro Thr Thr Lys Pro Ala Lys Ala Glu Val Glu Ser Ser
                      485                      490                      495
Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys
                      500                      505                      510
Pro Thr Thr Ala Ser Ser Glu Thr Thr Ile Asp Val Val Gln Thr Ser
                      515                      520                      525
Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn
530                      535                      540
Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Glu Asn Asn Lys Asn
545                      550                      555                      560
Thr Gln Glu Asn Lys Ala Lys Ser
                      565

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&lt;210&gt; 24

&lt;211&gt; 568

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 24

```

Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
1                      5                      10                      15
Ala Val Ala Ser Pro Ser Thr Thr Thr Glu Lys Ala Pro Glu Ala Lys
                      20                      25                      30
Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro
                      35                      40                      45
Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro
50                      55                      60
Lys Glu Thr Lys Glu Val Lys Pro Ala Thr Lys Ala Asp Asn Asn Thr
65                      70                      75                      80
Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala
                      85                      90                      95
Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe
                      100                      105                      110
Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser
115                      120                      125
Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile
130                      135                      140
Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr
145                      150                      155                      160

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Glu Gly Asn Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val  
 165 170 175  
 Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala  
 180 185 190  
 Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr  
 195 200 205  
 Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp  
 210 215 220  
 Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ser Pro  
 225 230 235 240  
 Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys  
 245 250 255  
 Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys  
 260 265 270  
 Leu Glu Glu Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile  
 275 280 285  
 Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu  
 290 295 300  
 Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser  
 305 310 315 320  
 Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn  
 325 330 335  
 Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys  
 340 345 350  
 Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala  
 355 360 365  
 Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr  
 370 375 380  
 Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp  
 385 390 395 400  
 Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala  
 405 410 415  
 Asn Ala Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys  
 420 425 430  
 Lys Glu Thr Thr Pro Ala Thr Pro Ser Lys Pro Thr Thr Pro Pro Val  
 435 440 445  
 Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln  
 450 455 460  
 Ser Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys  
 465 470 475 480  
 Asp Lys Thr Pro Ala Thr Lys Pro Ala Lys Ala Glu Val Glu Ser Ser  
 485 490 495  
 Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys  
 500 505 510  
 Pro Thr Thr Ala Ser Ser Glu Thr Thr Ile Asp Val Val Gln Thr Ser  
 515 520 525  
 Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn  
 530 535 540  
 Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Glu Asn Asn Lys Asn  
 545 550 555 560  
 Thr Gln Glu Asn Lys Ala Lys Ser  
 565

&lt;210&gt; 25

&lt;211&gt; 568

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 25

```

Ala Glu Glu Thr Gly Gly Thr Ile Thr Glu Thr Gln Pro Lys Thr Glu
 1           5           10           15
Ala Val Ala Ser Pro Thr Thr Thr Thr Glu Lys Ala Pro Glu Ala Lys
          20           25           30
Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Ala Ala Pro
          35           40           45
Thr Thr Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro
 50           55           60
Asn Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ser Asp Asn Asn Thr
65           70           75           80
Tyr Pro Ile Leu Asn Glu Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala
          85           90           95
Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe
          100          105          110
Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser
          115          120          125
Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile
          130          135          140
Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr
145          150          155          160
Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val
          165          170          175
Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala
          180          185          190
Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr
          195          200          205
Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp
210          215          220
Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro
225          230          235          240
Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys
          245          250          255
Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys
          260          265          270
Leu Glu Glu Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile
          275          280          285
Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu
          290          295          300
Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser
305          310          315          320
Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn
          325          330          335
Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys
          340          345          350
Asp Phe Met Val Glu Gly Glu Arg Val Arg Thr Ile Ser Lys Asp Ala
          355          360          365
Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr
          370          375          380

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Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp
385                      390                      395                      400
Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala
                      405                      410                      415
Asn Ala Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys
                      420                      425                      430
Lys Glu Thr Thr Pro Ala Thr Pro Ser Lys Pro Thr Thr Ala Pro Val
                      435                      440                      445
Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln
                      450                      455                      460
Ser Pro Ser Val Glu Lys Glu Ile Asp Ala Ser Ser Glu Ser Gly Lys
465                      470                      475                      480
Asp Lys Thr Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser
                      485                      490                      495
Ser Thr Thr Pro Thr Lys Val Val Ser Ala Thr Gln Asn Val Ala Lys
                      500                      505                      510
Pro Thr Ser Ala Ser Ser Glu Thr Thr Lys Gly Val Val Gln Thr Ser
                      515                      520                      525
Ala Gly Ser Ser Glu Ala Lys Asp Asn Ala Pro Leu Gln Lys Ala Asn
530                      535                      540
Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn
545                      550                      555                      560
Thr Gln Glu Asn Lys Ala Lys Ser
                      565

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&lt;210&gt; 26

&lt;211&gt; 568

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 26

```

Ala Glu Glu Thr Gly Gly Thr Ile Thr Glu Thr Gln Pro Lys Thr Glu
1      5      10      15
Ala Val Ala Ser Pro Thr Thr Thr Thr Glu Lys Ala Pro Glu Ala Lys
20      25      30
Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Val Ala Pro
35      40      45
Thr Thr Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro
50      55      60
Asn Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ser Asp Asn Asn Thr
65      70      75      80
Tyr Pro Ile Leu Asn Glu Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala
85      90      95
Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe
100     105     110
Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser
115     120     125
Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile
130     135     140
Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr
145     150     155     160

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Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val
				165					170					175	
Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala
			180					185					190		
Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr
		195					200					205			
Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp
	210				215						220				
Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro
225				230						235					240
Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys
			245						250					255	
Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys
			260					265					270		
Leu	Glu	Glu	Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile
		275					280					285			
Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu
	290				295						300				
Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser
305				310						315					320
Met	Met	Asp	Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn
			325						330					335	
Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys
			340				345						350		
Asp	Phe	Met	Val	Glu	Gly	Glu	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala
	355						360					365			
Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr
	370					375					380				
Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val	His	Val	Lys	Thr	Ile	Asp	Tyr	Asp
385				390						395					400
Gly	Gln	Tyr	His	Val	Arg	Ile	Val	Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala
			405						410					415	
Asn	Ala	Asp	Lys	Ser	Asn	Lys	Lys	Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys
			420					425					430		
Lys	Glu	Ala	Thr	Pro	Ala	Thr	Pro	Ser	Lys	Pro	Thr	Thr	Ala	Pro	Val
	435					440						445			
Glu	Lys	Glu	Ser	Gln	Lys	Gln	Asp	Ser	Gln	Lys	Asp	Asp	Asn	Lys	Gln
	450					455					460				
Ser	Pro	Ser	Val	Glu	Lys	Glu	Ile	Asp	Ala	Ser	Ser	Glu	Ser	Gly	Lys
465				470						475					480
Asp	Lys	Thr	Pro	Ala	Thr	Lys	Pro	Ala	Lys	Gly	Glu	Val	Glu	Ser	Ser
			485						490					495	
Ser	Thr	Thr	Pro	Thr	Lys	Val	Val	Ser	Ala	Thr	Gln	Asn	Val	Ala	Lys
			500					505					510		
Pro	Thr	Ser	Ala	Ser	S										

<210> 27  
<211> 570

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 27

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Met Gly Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys
 1           5           10           15
Thr Glu Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu
          20           25           30
Thr Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu
          35           40           45
Ala Pro Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys
          50           55           60
Ala Pro Lys Glu Thr Lys Glu Val Lys Pro Ala Lys Ala Thr Asn
65          70          75          80
Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn
          85          90          95
Pro Ala Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile
          100         105         110
Asp Phe Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr
          115         120         125
Ala Ser Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro
          130         135         140
Glu Ile Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu
145         150         155         160
Val Tyr Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp
          165         170         175
Thr Val Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr
          180         185         190
Lys Ala Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu
          195         200         205
Lys Tyr Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser
          210         215         220
Ala Asp Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu
225         230         235         240
Ala Pro Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu
          245         250         255
Asn Lys Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys
          260         265         270
Lys Lys Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser
          275         280         285
Ala Ile Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr
          290         295         300
Asp Leu Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn
305         310         315         320
Glu Ser Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met
          325         330         335
Leu Asn Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr
          340         345         350
Trp Lys Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys
          355         360         365
Asp Ala Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly
          370         375         380

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Lys Thr Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp  
 385 390 395 400  
 Tyr Asp Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr  
 405 410 415  
 Lys Ala Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser  
 420 425 430  
 Ala Lys Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser  
 435 440 445  
 Pro Val Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn  
 450 455 460  
 Lys Gln Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser  
 465 470 475 480  
 Gly Lys Gly Val Thr Leu Ala Thr Lys Pro Thr Lys Gly Glu Val Glu  
 485 490 495  
 Ser Ser Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val  
 500 505 510  
 Ala Lys Pro Thr Thr Gly Ser Ser Lys Thr Thr Lys Asp Val Val Gln  
 515 520 525  
 Thr Ser Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys  
 530 535 540  
 Ala Asn Ile Lys His Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn  
 545 550 555 560  
 Lys Asn Thr Gln Glu Asn Lys Ala Lys Ser  
 565 570

&lt;210&gt; 28

&lt;211&gt; 654

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> SEQ ID NO: 2 modified to contain a glycine after  
 the amino terminus methionine and a carboxyl  
 His-Tag

&lt;400&gt; 28

Met Gly Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg  
 1 5 10 15  
 Lys Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu  
 20 25 30  
 Leu Met Ser Asn Gly Glu Ala Gln Ala Ala Ala Glu Thr Gly Gly  
 35 40 45  
 Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr  
 50 55 60  
 Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val  
 65 70 75 80  
 Ser Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu  
 85 90 95  
 Ala Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val  
 100 105 110  
 Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln  
 115 120 125  
 Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His  
 130 135 140

Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe	Glu	Met	Lys	Lys	Lys	Asp
145					150					155					160
Gly	Thr	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser	Ser	Val	Lys	Pro	Ala	Arg
				165					170						175
Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile	Glu	Leu	Gly	Leu	Gln	Ser
			180					185					190		
Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr	Glu	Gly	Asp	Lys	Lys	Leu
		195					200					205			
Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val	Lys	Asp	Tyr	Ala	Tyr	Ile
	210					215					220				
Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	Val	Lys	Ile	Val	Ser	Ser
225					230					235					240
Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	Asp	Tyr	Thr	Leu	Met	Glu
			245						250					255	
Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	Lys	Phe	Lys	Thr	Glu	Glu
		260						265					270		
Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	Tyr	Lys	Lys	Ala	Lys	Thr
		275					280					285			
Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys	Ile	Gln	Asp	Lys	Leu	Pro
	290					295					300				
Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys	Leu	Glu	Asp	Thr	Lys	Lys
305					310					315					320
Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile	Thr	Glu	Phe	Gln	Asn	Val
			325						330					335	
Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu	Gln	Asp	Thr	Lys	Tyr	Val
			340					345					350		
Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser	Met	Met	Asp	Thr	Phe	Val
		355				360						365			
Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	Gly	Lys	Lys	Tyr	Met	Val
	370					375					380				
Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys	Asp	Phe	Met	Val	Glu	Gly
385				390						395					400
Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	Lys	Asn	Asn	Thr	Arg	Thr
			405						410					415	
Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr	Leu	Tyr	Asp	Ala	Ile	Val
		420						425					430		
Lys	Val	His	Val	Lys	Thr	Ile	Asp	Tyr	Asp	Gly	Gln	Tyr	His	Val	Arg
		435					440					445			
Ile	Val	Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala	Asn	Thr	Asp	Lys	Ser	Asn
	450					455					460				
Lys	Lys	Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys	Lys	Glu	Ala	Thr	Pro	Ala
465					470					475					480
Thr	Pro	Ser	Lys	Pro	Thr	Pro	Ser	Pro	Val	Glu	Lys	Glu	Ser	Gln	Lys
			485						490					495	
Gln	Asp	Ser	Gln	Lys	Asp	Asp	Asn	Lys	Gln	Leu	Pro	Ser	Val	Glu	Lys
			500					505					510		
Glu	Asn	Asp	Ala	Ser	Ser	Glu	Ser	Gly	Lys	Asp	Lys	Thr	Pro	Ala	Thr
		515					520					525			
Lys	Pro	Thr	Lys	Gly	Glu	Val	Glu	Ser	Ser	Ser	Thr	Thr	Pro	Thr	Lys
	530					535					540				
Val	Val	Ser	Thr	Thr	Gln	Asn	Val	Ala	Lys	Pro	Thr	Thr	Ala	Ser	Ser
545					550					555					560
Lys	Thr	Thr	Lys	Asp	Val	Val	Gln	Thr	Ser	Ala	Gly	Ser	Ser	Glu	Ala
				565					570					575	

Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp  
 580 585 590  
 Gly His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala  
 595 600 605  
 Lys Ser Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu  
 610 615 620  
 Pro Leu Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu  
 625 630 635 640  
 Pro Arg Lys Arg Lys Asn Leu Glu His His His His His His  
 645 650

<210> 29  
 <211> 1962  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Full length ORF0657n + Carboxyl His-Tag

<400> 29  
 atgaacaaac agcaaaaaga attttaatca ttttattcaa ttagaaagtc atcactaggc 60  
 gttgcatctg tagcaattag tacactttta ttattaatgt caaatggcga agcacaagca 120  
 gcagctgaag aaacagggtgg tacaataaca gaagcacaac caaaaactga agcagttgca 180  
 agtccaacaa caacatctga aaaagctcca gaaactaaac cagtagctaa tgctgtctca 240  
 gtatctaata agaagttga ggccctact tctgaaacaa aagaagctaa agaagttaaa 300  
 gaagttaaag cccctaagga acaaaaagaa gttaaccag cagcaaaagc cactaacaat 360  
 acatatccta ttttgaatca ggaacttaga gaagcgatta aaaaccctgc aataaaagac 420  
 aaagatcata gcgcaccaaa ctctcgtcca attgattttg aaatgaaaaa gaaagatgga 480  
 actcaacagt tttatcatta tgcaagttct gttaaaccctg ctagagttat tttcactgat 540  
 tcaaaaccag aaattgaatt aggattacaa tcaggtcaat tttggagaaa atttgaagtt 600  
 tatgaagggtg acaaaaagtt gccaatataa ttagtatcat acgatactgt taaagattat 660  
 gcttacattc gcttctctgt atcaaacgga acaaaagctg ttaaaattgt tagttcaaca 720  
 cacttcaata acaaaagaaga aaaatacgat tacacattaa tggaattcgc acaaccaatt 780  
 tataacagtg cagataaatt caaaactgaa gaagattata aagctgaaaa attattagcg 840  
 ccatataaaa aagcgaaaac actagaaaga caagtttatg aattaaataa aattcaagat 900  
 aaacttcctg aaaaattaaa ggctgagtag aagaagaaat tagaggatac aaagaaagct 960  
 ttagatgagc aagtgaatc agctattact gaattccaaa atgtacaacc aacaaatgaa 1020  
 aaaatgactg atttacaaga tacaaaatat gttgtttatg aaagtgttga gaataacgaa 1080  
 tctatgatgg atacttttgt taaacaccct attaaaacag gtatgcttaa cggcaaaaaa 1140  
 tatatgggtca tggaaactac taatgacgat tactggaaag atttcatggt tgaagggtcaa 1200  
 cgtgttagaa ctataagcaa agatgctaaa aataatacta gaacaattat tttcccatat 1260  
 gttgaaggta aaactctata tgatgctatc gttaaagttc acgtaaaaac gattgattat 1320  
 gatggacaat accatgtcag aatcgttgat aaagaagcat ttacaaaagc caataccgat 1380  
 aaatctaaca aaaaagaaca acaagataac tcagctaaga aggaagctac tccagctacg 1440  
 cctagcaaac caacaccatc acctgttgaa aaagaatcac aaaaacaaga cagccaaaaa 1500  
 gatgacaata aacaattacc aagtgttgaa aaagaaaatg acgcatctag tgagtcagggt 1560  
 aaagacaaaa cgctgctac aaaaccaact aaagggtgaag tagaatcaag tagtacaact 1620  
 ccaactaagg tagtatctac gactcaaaat gttgcaaaac caacaactgc ttcatacaaaa 1680  
 acaacaaaag atgttgttca aacttcagca ggttctagcg aagcaaaaaga tagtgctcca 1740  
 ttacaaaaag caaacattaa aaacacaaat gatggacaca ctcaaagcca aaacaataaa 1800  
 aatacacaag aaaataaagc aaaatcatta ccacaaactg gtgaagaatc aaataaagat 1860  
 atgacattac cattaatggc attattagct ttaagtagca tcgttgcatt cgtattacct 1920  
 agaaaacgta aaaacctcga gcaccaccac caccaccact ga 1962

<210> 30

&lt;211&gt; 1737

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH + Carboxyl His-Tag

&lt;400&gt; 30

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atgaacgctg aagaaacagg tggtaacaat acagaagcac aacaaaaaac tgaagcagtt 60
gcaagtccaa caacaacatc tgaaaaagct ccagaaacta aaccagtagc taatgctgtc 120
tcagtatcta ataaagaagt tgaggccctt acttctgaaa caaaagaagc taaagaagtt 180
aaagaagtta aagcccctaa ggaaacaaaa gaagttaaac cagcagcaaa agccactaac 240
aatacatatc ctatttttgaa tcaggaactt agagaagcga ttaaaaaccc tgcaataaaa 300
gacaaagatc atagcgcacc aaactctcgt ccaattgatt ttgaaatgaa aaagaaagat 360
ggaactcaac agtttttatca ttatgcaagt tctgttaaac ctgctagagt tattttctact 420
gattcaaaac cagaaattga attaggatta caatcagggtc aattttggag aaaatttgaa 480
gtttatgaag gtgacaaaaa gttgccaaat aaatttagtat catacgatac tgttaaagat 540
tatgcttaca ttcgcttctc tgtatcaaac ggaacaaaag ctgttaaaat tgttagttca 600
acacacttca ataacaaaga agaaaaatac gattacacat taatggaatt cgcacaacca 660
atttataaca gtgcagataa attcaaaact gaagaagatt ataaagctga aaaattatta 720
gcgccatata aaaaagcgaa aacactagaa agacaagttt atgaattaaa taaaattcaa 780
gataaacttc ctgaaaaatt aaaggctgag tacaagaaga aattagagga tacaagaaa 840
gcttttagatg agcaagtga atcagctatt actgaattcc aaaatgtaca accaacaaat 900
gaaaaaatga ctgattttaca agatacaaaa tatgttgttt atgaaagtgt tgagaataac 960
gaatctatga tggatacttt tgtaaacac cctattaaaa caggtagtgc taacggcaaa 1020
aaatatatgg tcatggaaac tactaatgac gattactgga aagatttcat gggtgaaggt 1080
caacgtgtta gaactataag caaagatgct aaaaataata ctagaacaat tattttccca 1140
tatgttgaag gtaaaactct atatgatgct atcgttaaag ttcacgtaaa aacgattgat 1200
tatgatggac aataccatgt cagaatcggt gataaagaag catttacaaa agccaatacc 1260
gataaatcta acaaaaaaga acaacaagat aactcagcta agaaggaagc tactccagct 1320
acgcctagca aaccaacacc atcacctggt gaaaaagaat cacaaaaaca agacagccaa 1380
aaagatgaca ataaacaatt accaagtgtt gaaaaagaaa atgacgcac tagtgagtca 1440
ggtaaagaca aaacgcctgc tacaaaacca actaaagggtg aagtagaatc aagtagtaca 1500
actccaacta aggtagtatc tacgactcaa aatggtgcaa aaccaacaac tgcttcatca 1560
aaaacaacaa aagatgttgt tcaaaacttca gcaggttcta gcgaagcaaa agatagtgc 1620
ccattacaaa aagcaaacat taaaaacaca aatgatggac acactcaaag ccaaaacaat 1680
aaaaatacac aagaaaataa agcaaaatca ctcgagcacc accaccacca ccactga 1737

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&lt;210&gt; 31

&lt;211&gt; 1941

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Encodes SEQ ID NO: 28 without a carboxyl His-Tag  
and is codon optimized for yeast expression

&lt;400&gt; 31

```

atgggtaaca agcaacaaaa ggaattcaag tctttctact ccattagaaa gtcttccttg 60
ggtgttgctt ctgtcgctat ctccaccttg ttgttggtga tgtctaacgg tgaagctcaa 120
gctgctgctg aagaaactgg tggtaacca actgaagctc aaccaaagac cgaagctgtc 180
gcttcccca acaactacct tgaaaaggct ccagaaacta agccagttgc taacgctgtc 240
tccgtttcta acaaggaagt cgaagctcca acctccgaaa ctaaggaagc taaggaagtt 300
aaggaagtca aggtccaaa ggaaactaag gaagtcaagc cagctgctaa ggctaccaac 360
aacacttacc caattttgaa ccaagaattg agagaagcta ttaagaaccc agctatcaag 420

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gacaaggacc actccgctcc aaactctaga ccaatcgact tcgaaatgaa gaagaaggac 480
ggtacccaac aattctacca ctacgcgtcc tctgtcaagc cagctagagt tattttcacc 540
gactctaagc cagaaatcga attgggtttg caatccggtc aattctggag aaagttcgaa 600
gtctacgaag gtgacaagaa gttgccaatt aagttggttt cctacgacac cgtcaaggac 660
tacgcttaca tcagattctc cgtttctaac ggtactaagg ctgtcaagat tgtctcttcc 720
accacttca acaacaagga agaaaagtac gactacactt tgatggaatt cgctcaacca 780
atttacaact ctgctgacaa gttcaagacc gaagaagact acaaggctga aaagttgttg 840
gctccataca agaaggctaa gactttggaa agacaagttt acgaattgaa caagatccaa 900
gacaagttgc cagaaaagtt gaaggctgaa tacaagaaga agttggaaga caccaagaag 960
gctttggacg aacaagtcaa gtccgctatc accgaattcc aaaacggtca accaactaac 1020
gaaaagatga ctgacttgca agacactaag tacgtcgtct acgaatccgt cgaaaacaac 1080
gaatccatga tggacacctt cgtaagcac ccaattaaga ctggtatgtt gaacggtaag 1140
aagtacatgg tcatggaaac cactaacgac gactactgga aggacttcat ggttgaaggt 1200
caaagagtca gaaccatctc caaggacgct aagaacaaca ctagaacat tatcttccca 1260
tacgttgaag gtaagacttt gtacgacgct atcgtcaagg ttcacgtcaa gactattgac 1320
tacgacggtc aataccacgt tagaattgtt gacaaggaag ctttcaccaa ggctaacacc 1380
gacaagtcca acaagaagga acaacaagac aactctgcta agaaggaagc taccacagt 1440
acccctcta agccaacccc atctccagtt gaaaaggaat ctcaaaagca agactcccaa 1500
aaggacgaca acaagcaatt gccatccgtc gaaaaggaaa acgacgcgtc ttctgaatcc 1560
ggtaaggaca agactccagc taccaagcca actaagggtg aagttgaatc ttctctact 1620
actccaacca aggttgtctc cactacccaa aacgtcgcta agccaactac cgcttcttcc 1680
aagactacca aggacgttgt ccaaacttct gctggttcct ctgaagctaa ggactctgct 1740
ccattgcaaa aggctaacat caagaacacc aacgacggtc acaccaatc ccaaaacaac 1800
aagaacactc aagaaaacaa ggctaagtct ttgccacaaa ccggtgaaga atccaacaag 1860
gacatgacct tgccattgat ggctttgttg gctttgtctt ccatcgttgc tttcgtcttg 1920
ccaagaaga gaaagaacta a

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<210> 32

<211> 1710

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes SEQ ID NO: 3 and is codon optimized for yeast expression

<400> 32

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atgggtgaag aaactgggtg taccaacact gaagctcaac caaagaccga agctgtcgct 60
tcccaacca ctacctctga aaagggtcca gaaactaagc cagttgctaa cgctgtctcc 120
gtttctaaca aggaagtcca agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
acttaccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aatgaagaa gaaggacggt 360
acccaacaat tctaccacta cgcgctctct gtcaagccag ctagagttat tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatatag ttggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttcacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tggaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggct 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtgaagaag 1020
tacatggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080

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agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1200
gacgggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caacccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaaag 1380
gacgacaaca agcaattgcc atccgctcga aagggaaaacg acgctgtctc tgaatccggg 1440
aaggacaaga ctccagctac caagccaact aaggggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac tacccaaaac gtcgctaagc caactaccgc ttcttccaag 1560
actaccaagg acgttgttcca aacttctgct gggtcctctg aagctaagga ctctgctcca 1620
ttgcaaaagg ctaacatcaa gaacaccaac gacggtcaca cccaatccca aaacaacaag 1680
aacactcaag aaaacaaggc taagtcttaa 1710

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&lt;210&gt; 33

&lt;211&gt; 1341

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Encodes SEQ ID NO: 1 and is codon optimized for yeast expression

&lt;400&gt; 33

```

atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgtc 60
tcccacaaca ctacctctga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 120
gtttctaaca aggaagtcga agtccaact tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccacgc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360
accaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccgggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatatag ttgggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttcacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tggaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggt 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtagaag 1020
tacatggtca tggaaccac taacgacgac tactggaagg acttcatggt tgaaggtaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1200
gacgggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caacccata a 1341

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&lt;210&gt; 34

&lt;211&gt; 1710

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Encodes SEQ ID NO: 7 containing an amino terminus methionine and is codon optimized for yeast expression

&lt;400&gt; 34

```

atgggtgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60
tccccaacca ctacctctga aaagggtcca gaaactaagc cagttgctaa cgctgtctcc 120
gttttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360
acccaacaat tctaccacta cgcgtcctct gtcaagccag ctagagtta tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccgggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatgaag ttggtttctt acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tgggaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggct 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tgggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgtatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagta gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
tacatggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaaggtaa 1080
agagtcagaa ccattctcaa ggacgctaag aacaacacta gaaccattat ctctccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaaggttc acgtcaagac tattgactac 1200
gacggtcaat accacgttag aattgttgac aagggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccattctaagc caacccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgctcttc tgaatccggt 1440
aagggtgtca ctttgggtac caagccaact aagggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac tacccaaaac gtcgctaagc caactaccgg ttcttccaag 1560
actaccaagg acgttggtcca aacttctgct ggttctctg aagctaagga ctctgtctca 1620
ttgcaaaagg ctaacatcaa gcacaccaac gacggtcaca cccaatccca aaacaacaag 1680
aacactcaag aaaacaaggc taagtcttaa 1710

```

&lt;210&gt; 35

&lt;211&gt; 1710

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Encodes SEQ ID NO: 7 containing an amino terminus methionine and is codon optimized for yeast expression

&lt;400&gt; 35

```

atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60
tccccaacca ctacctctga aaagggtcca gaaactaagc cagttgctaa cgctgtctcc 120
gttttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360
acccaacaat tctaccacta cgcgtcctct gtcaagccag ctagagtta tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccgggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatgaag ttggtttctt acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tgggaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggct 720

```

```

ccatacaaga aggctaagac tttggaaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
tacatgggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1200
gacgggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aagggaaaacg acgctcttc tgaatccggt 1440
aagggcggtca ctttgggtac caagccaact aaggggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac tacccaaaac gtcgctaagc caactaccgg ttcttccaag 1560
actaccaagg acgttgtcca aacttctgct gggttcctctg aagctaagga ctctgtctca 1620
ttgcaaaagg ctaacatcaa gcacaccaac gacggtcaca cccaatccca aaacaacaag 1680
aacactcaag aaaacaaggc taagtcttaa 1710

```

<210> 36

<211> 1710

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes SEQ ID NO: 7 containing an amino terminus  
methionine and is codon optimized for yeast  
expression

<400> 36

```

atggctgaag aaactgggtg taccaacact gaagctcaac caaagaccga agctgtcgtc 60
tccccaacca ctacctctga aaagggtcca gaaactaagc cagttgctaa cgctgtctcc 120
gtttctaaca aggaagtcca agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360
acccaacaat tctaccacta cgcgctctct gtcaagccag ctagagttat tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccgggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatgaag ttggtttctc acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttcacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tgggaattcg tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttgggt 720
ccatacaaga aggctaagac tttggaaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
tacatgggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1200
gacgggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aagggaaaacg acgctcttc tgaatccggt 1440
aaggggtgta ctttgggtac caagccaact aaggggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac tacccaaaac gtcgctaagc caactaccgg ttcttccaag 1560

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actaccaagg acgttggtcca aactttctgct ggttcctctg aagctaagga ctctgctcca 1620
ttgcaaaagg ctaacatcaa gcacaccaac gacggtcaca cccaatccca aaacaacaag 1680
aacactcaag aaaacaaggc taagtcttaa 1710

```

<210> 37

<211> 1710

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes SEQ ID NO: 7 containing an amino terminus methionine and is codon optimized for yeast expression

<400> 37

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atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60
tccccaaacca ctacctctga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 120
gttttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360
acccaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccgggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatgaag ttggtttctt acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tgggaattcg tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggct 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tgggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgctga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
tacatgggtc tggaaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1200
gacgggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380
gacgacaaca agcaattgcc atccgctcga aaggaaaacg acgctcttc tgaatccggt 1440
aagggcggtta ctttgggtac caagccaact aaggggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac tacccaaaac gtcgctaagc caactaccgg ttcttccaag 1560
actaccaagg acgttggtcca aacttctgct ggttcctctg aagctaagga ctctgctcca 1620
ttgcaaaagg ctaacatcaa gcacaccaac gacggtcaca cccaatccca aaacaacaag 1680
aacactcaag aaaacaaggc taagtcttaa 1710

```

<210> 38

<211> 1710

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes SEQ ID NO: 7 containing an amino terminus methionine and is codon optimized for yeast expression

&lt;400&gt; 38

```

atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60
tccccaacca ctacctctga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 120
gttttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360
acccaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccgggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatgaag ttggtttctt acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tgggaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggct 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tgggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
tacatggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtt acgtcaagac tattgactac 1200
gacggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac ccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aagggaaacg acgctcttc tgaatccggt 1440
aagggtgtca ctttagctac caagccaact aagggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac taccaaaaac gtcgctaagc caactaccg tcttccaaag 1560
actaccaagg acgttgtcca aacttctgct gggtctctctg aagctaagga ctctgtctca 1620
ttgcaaaagg ctaacatcaa gcacaccaac gacggtcaca cccaatccca aaacaacaag 1680
aacactcaag aaaacaaggc taagtcttaa 1710

```

&lt;210&gt; 39

&lt;211&gt; 1710

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Encodes SEQ ID NO: 7 containing an amino terminus methionine and is codon optimized for yeast expression

&lt;400&gt; 39

```

atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60
tccccaacca ctacctctga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 120
gttttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360
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tctaagccag aaatcgaatt gggtttgcaa tccgggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatgaag ttggtttctt acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tgggaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggct 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780

```

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aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtagaag 1020
tacatggtca tggaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatat 1140
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gacggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgctcttc tgaatccggt 1440
aagggtgtca ctttggttac caagccaact aagggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac tacccaaaac gtcgctaagc caactaccgg ctcttccaag 1560
actaccaagg acgttgtcca aacttctgct ggttcctctg aagctaagga ctctgctcca 1620
ttgcaaaagg ctaacatcaa gcacaccaac gacggtcaca cccaatcca aaacaacaag 1680
aacactcaag aaaacaaggc taagtcttaa 1710

```

&lt;210&gt; 40

&lt;211&gt; 1710

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Encodes SEQ ID NO: 7 containing an amino terminus  
methionine and is codon optimized for yeast  
expression

&lt;400&gt; 40

```

atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60
tcccaacca ctacctctga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 120
gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
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ccaaccaagg ttgtctccac tacccaaaac gtcgctaagc caactaccgg ttcttccaag 1560
actaccaagg acgttgtcca aacttctgct ggttcctctg aagctaagga ctctgctcca 1620

```

ttgcaaaagg ctaacatcaa gcacaccaac gacgggcaca cccaatccca aaacaacaag 1680  
aacactcaag aaaacaaggc taagtcttaa 1710

<210> 41

<211> 1710

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes SEQ ID NO: 7 containing an amino terminus  
methionine and is codon optimized for yeast  
expression

<400> 41

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atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60
tccccaacca ctacctctga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 120
gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccacagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggg 360
accaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccgggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatataag ttggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggg actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tggaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttggtggct 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
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gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1200
gacgggtcaat accacggttag aattggtgac aagggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaaatctc aaaagcaaga ctcccaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgctcttc tgaatccggg 1440
aagggtgtta ctttgggtac caagccaact aagggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac taccctaaac gtcgctaagc caactaccgg ctcttccaag 1560
actaccaagg acgttggtcca aacttctgct gggtcctctg aagctaagga ctctgtctca 1620
ttgcaaaagg ctaacatcaa gcacaccaac gacgggcaca cccaatccca aaacaacaag 1680
aacactcaag aaaacaaggc taagtcttaa 1710
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<210> 42

<211> 481

<212> PRT

<213> Artificial Sequence

<220>

<223> ORF0657nI+

<400> 42

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1           5           10           15
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Glu Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu Thr  
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 Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala  
 35 40 45  
 Pro Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala  
 50 55 60  
 Pro Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn  
 65 70 75 80  
 Thr Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro  
 85 90 95  
 Ala Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp  
 100 105 110  
 Phe Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala  
 115 120 125  
 Ser Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu  
 130 135 140  
 Ile Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val  
 145 150 155 160  
 Tyr Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr  
 165 170 175  
 Val Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys  
 180 185 190  
 Ala Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys  
 195 200 205  
 Tyr Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala  
 210 215 220  
 Asp Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala  
 225 230 235 240  
 Pro Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn  
 245 250 255  
 Lys Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys  
 260 265 270  
 Lys Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala  
 275 280 285  
 Ile Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp  
 290 295 300  
 Leu Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu  
 305 310 315 320  
 Ser Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu  
 325 330 335  
 Asn Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp  
 340 345 350  
 Lys Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp  
 355 360 365  
 Ala Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys  
 370 375 380  
 Thr Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr  
 385 390 395 400  
 Asp Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys  
 405 410 415  
 Ala Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala  
 420 425 430  
 Lys Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro  
 435 440 445

Val Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys  
 450 455 460  
 Gln Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly  
 465 470 475 480  
 Lys

<210> 43  
 <211> 1452  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Encodes SEQ ID NO: 42 and is codon optimized for  
 yeast expression

<400> 43  
 atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60  
 tcccaacca ctacctctga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 120  
 gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180  
 gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240  
 acttacccaa ttttgaacca agaattgaga gaagctatta agaaccacgc tatcaaggac 300  
 aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggg 360  
 acccaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 420  
 tctaagccag aaatcgaatt gggtttgcaa tccgggtcaat tctggagaaa gttcgaagtc 480  
 tacgaagggtg acaagaagtt gccaatataag ttggtttcct acgacaccgt caaggactac 540  
 gcttacatca gattctccgt ttctaacggg actaaggctg tcaagattgt ctcttcacc 600  
 cacttcaaca acaaggaaga aaagtacgac tacactttga tggaattcgc tcaaccaatt 660  
 tacaactctg ctgacaagtt caagaccgaa gaagactaca aggttgaaaa gttgttggt 720  
 ccatacaaga aggttaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780  
 aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaaggct 840  
 ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900  
 aagatgactg acttgcaaga cactaagtag gtcgtctacg aatccgtcga aaacaacgaa 960  
 tccatgatgg acaccttcgt taagcaccca attagactg gtatgttgaa cggtagaag 1020  
 tacatggtca tggaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080  
 agagtcagaa ccattctcaa ggacgctaag aacaacacta gaaccattat cttcccatc 1140  
 gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1200  
 gacggtcaat accacgtag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260  
 aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320  
 ccattctaagc caacccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380  
 gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgcgtcttc tgaatccggt 1440  
 aagtaaggat cc 1452

<210> 44  
 <211> 605  
 <212> PRT  
 <213> ORF0657nG

<400> 44  
 Met Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr  
 1 5 10 15  
 Glu Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu Thr  
 20 25 30  
 Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala  
 35 40 45

Pro Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala  
 50 55 60  
 Pro Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn  
 65 70 75 80  
 Thr Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro  
 85 90 95  
 Ala Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp  
 100 105 110  
 Phe Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala  
 115 120 125  
 Ser Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu  
 130 135 140  
 Ile Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val  
 145 150 155 160  
 Tyr Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr  
 165 170 175  
 Val Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys  
 180 185 190  
 Ala Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys  
 195 200 205  
 Tyr Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala  
 210 215 220  
 Asp Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala  
 225 230 235 240  
 Pro Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn  
 245 250 255  
 Lys Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys  
 260 265 270  
 Lys Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala  
 275 280 285  
 Ile Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp  
 290 295 300  
 Leu Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu  
 305 310 315 320  
 Ser Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu  
 325 330 335  
 Asn Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp  
 340 345 350  
 Lys Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp  
 355 360 365  
 Ala Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys  
 370 375 380  
 Thr Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr  
 385 390 395 400  
 Asp Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys  
 405 410 415  
 Ala Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala  
 420 425 430  
 Lys Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro  
 435 440 445  
 Val Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys  
 450 455 460  
 Gln Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly  
 465 470 475 480

Lys	Asp	Lys	Thr	Pro	Ala	Thr	Lys	Pro	Thr	Lys	Gly	Glu	Val	Glu	Ser
				485					490					495	
Ser	Ser	Thr	Thr	Pro	Thr	Lys	Val	Val	Ser	Thr	Thr	Gln	Asn	Val	Ala
			500					505					510		
Lys	Pro	Thr	Thr	Ala	Ser	Ser	Lys	Thr	Thr	Lys	Asp	Val	Val	Gln	Thr
		515					520					525			
Ser	Ala	Gly	Ser	Ser	Glu	Ala	Lys	Asp	Ser	Ala	Pro	Leu	Gln	Lys	Ala
	530					535					540				
Asn	Ile	Lys	Asn	Thr	Asn	Asp	Gly	His	Thr	Gln	Ser	Gln	Asn	Asn	Lys
545					550					555					560
Asn	Thr	Gln	Glu	Asn	Lys	Ala	Lys	Ser	Leu	Pro	Gln	Thr	Gly	Glu	Glu
				565					570					575	
Ser	Asn	Lys	Asp	Met	Thr	Leu	Pro	Leu	Met	Ala	Leu	Leu	Ala	Leu	Ser
			580					585					590		
Ser	Ile	Val	Ala	Phe	Val	Leu	Pro	Arg	Lys	Arg	Lys	Asn			
		595					600					605			

&lt;210&gt; 45

&lt;211&gt; 1818

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Encodes SEQ ID NO: 44 containing an amino terminus  
methionine and is codon optimized for yeast  
expression

&lt;400&gt; 45

```

atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60
tccccaacca ctacctctga aaagggtcca gaaactaagc cagttgctaa cgctgtctcc 120
gtttctaaca aggaagtcca agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360
accaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccgggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatataag ttggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tgggaattcg tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggct 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
tacatggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatat 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1200
gacggtcaat accacgtag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccgctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgctcttc tgaatccggt 1440
aaggacaaga ctccagctac caagccaact aagggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac tacccaaaac gtcgctaagc caactaccgc ttcttccaag 1560
actaccaagg acgttgtcca aacttctgct ggttcctctg aagctaagga ctctgctcca 1620

```



```

ttgcaaaagg ctaacatcaa gaacaccaac gacggtcaca cccaatccca aaacaacaag 1680
aacactcaag aaaacaaggc taagtctttg ccacaaaccg gtgaagaatc caacaaggac 1740
atgaccttgc cattgatggc tttgttggtt ttgtcttcca tcgttgcttt cgtcttgcca 1800
agaaagagaa agaactaa                                     1818

```

<210> 46

<211> 1710

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes SEQ ID NO: 17 containing an amino terminus  
methionine and is codon optimized for yeast  
expression

<400> 46

```

atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctttggct 60
tccccaaaca ctaccactga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 120
gttttctaaca aggaagtcca agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggct gtcaagccag ctgctaaggc tgacaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccacgc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa ggaaaacggt 360
gaacaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccgggtcaat tctggagaaa gttcgaagtc 480
tacgaaggtg acaagaagtt gccaatgaag ttggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttcacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tgggaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggtt 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtag gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
tacatggtca tggaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatc 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtt acgtcaagac tattgactac 1200
gacggtcaat accacgttag aattgttgac aagggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggatctc aaaagcaaga ctcccaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgctccttc tgaatccggt 1440
aaggacaaga ctccagctac caagccagct aagggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac taccctaaac gtcgctaagc caactaccgc ttcttccaag 1560
actaccaagg acgttggtcca aacttctgct ggttcctctg aagctaagga ctctgtctca 1620
ttgcaaaagg ctaacatcaa gaacaccaac gacggtcaca cccaatccca aaacaacaag 1680
aacactcaag aaaacaaggc taagtcttaa                                     1710

```

<210> 47

<211> 1446

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes the SEQ ID NO: 17 I+ region, is codon  
optimized for yeast expression, and encodes a  
methionine initiation codon

&lt;400&gt; 47

```

atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctttggct 60
tccccaacca ctaccactga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 120
gttttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggct gtcaagccag ctgctaaggc tgacaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa ggaaaacggg 360
gaacaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccgggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatlaag ttggtttccct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggg actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tgggaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggct 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tgggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgctcg aaacaacgaa 960
tccatgatgg acaccttctg taagcaccca attagactg gtatgttgaa cggtaagaag 1020
tacatgggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080
agagtcagaa ccattctcaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtt acgtcaagac tattgactac 1200
gacgggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caacccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aagggaaaacg acgctgtctc tgaatccggg 1440
aagtaa 1446

```

&lt;210&gt; 48

&lt;211&gt; 1341

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Encodes the SEQ ID NO: 17 I region, is codon optimized for yeast expression, and encodes a methionine initiation codon

&lt;400&gt; 48

```

atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctttggct 60
tccccaacca ctaccactga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 120
gttttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggct gtcaagccag ctgctaaggc tgacaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa ggaaaacggg 360
gaacaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccgggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatlaag ttggtttccct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggg actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tgggaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggct 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tgggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgctcg aaacaacgaa 960

```

```

tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
tacatgggtca tggaaaccac taacgacgac tactggaagg acttcatggg tgaagggtcaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1200
gacgggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccata a                                     1341

```

<210> 49

<211> 1938

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes for full length ORF0657n containing SEQ ID

NO: 17 modified to contain a glycine afer the  
amino terminus methionine and is codon optimized  
for yeast expression

<400> 49

```

atgggtaaca agcaacaaaa ggaattcaag tctttctact ccattagaaa gtcttccttg 60
gggtgttgctt ctgtcgctat ctccaccttg ttgttggtga tgtctaacgg tgaaggtcaa 120
gctgctgaag aaactgggtgg taccaacact gaagctcaac caaagaccga agctttgggt 180
tccccaacca ctaccactga aaagggtcca gaaactaagc cagttgctaa cgctgtctcc 240
gtttctaaca aggaagtcca agctccaacc tccgaaacta aggaagctaa ggaagttaag 300
gaagtcaagg ctccaaagga aactaagggt gtcaagccag ctgctaaggc tgacaacaac 360
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 420
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa ggaaaacggg 480
gaacaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttat tttaccgac 540
tctaagccag aaatcgaaat gggtttgcaa tccgggtcaat tctggagaaa gttcgaagtc 600
tacgaagggtg acaagaaggt gccaatgaag ttgggtttcct acgacaccgt caaggactac 660
gcttacatca gattctccgt ttctaacggg actaagggtg tcaagattgt ctcttccacc 720
cacttcaaca acaaggaaga aaagtacgac tacactttga tggaattcgc tcaaccaatt 780
tacaactctg ctgacaaggt caagaccgaa gaagactaca aggctgaaaa gttgttggt 840
ccatacaaga aggtcaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 900
aagttgccag aaaagtggaa ggctgaatac aagaagaagt tggaagacac caagaaggct 960
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 1020
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 1080
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1140
tacatgggtca tggaaaccac taacgacgac tactggaagg acttcatggg tgaagggtcaa 1200
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1260
gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1320
gacgggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1380
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1440
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaaag 1500
gacgacaaca agcaattgcc atccgtcgaa aagggaaaacg acgcgtcttc tgaatccggg 1560
aaggacaaga ctccagctac caagccagct aagggtgaag ttgaatcttc ctctactact 1620
ccaaccaagg ttgtctccac tacccaaaac gtcgctaagc caactaccgc ttcttccaag 1680
actaccaagg acgttgtcca aacttctgct ggttcctctg aagctaagga ctctgctcca 1740
ttgcaaaaagg ctaacatcaa gaacaccaac gacgggtcaca cccaatccca aaacaacaag 1800
aacactcaag aaaacaaggc taagtctttg ccacaaaccg gtgaagaatc caacaaggac 1860
atgaccttgc cattgatggc tttgttggtt ttgtcttcca tcgttgcttt cgtcttgcca 1920
agaagagaa agaactaa                                     1938

```

<210> 50

&lt;211&gt; 1710

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Encodes SEQ ID NO: 20, is codon optimized for yeast expression, and encodes a methionine initiation codon

&lt;400&gt; 50

```

atggctgaag aaactgggtg taccaacact gaagctcaac caaagaccga agctgtcgct 60
tccccaacca ctacctctga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 120
gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggct gtcaagccag ctactaaggc tgacaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccacagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa ggaaaacggg 360
gaacaacaat tctaccacta cgcgtcctct gtcaagccag cttagagttat tttcaccgac 420
tctaagccag aaatcgaaatt gggtttgcaa tccgggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatgaag ttggtttctc acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggg actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tgggaattcg tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggct 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tgggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acggttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
tacatggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaaggtaaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatc 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1200
gacggtcaat accacgtagg aattgttgac aagggaagct tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgctgtctc tgaatccggt 1440
aaggacaaga ctccagctac caagccagct aagggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac tacccaaaac gtcgctaagc caactaccgc ttcttccaag 1560
actaccaagg acgttggtcca aacttctgct gggtcctctg aagctaagga ctctgtctca 1620
ttgcaaaaagg ctaacatcaa gaacaccaac gacggtcaca cccaatccca aaacaacaag 1680
aacactcaag aaaacaaggc taagtcttaa

```

&lt;210&gt; 51

&lt;211&gt; 1446

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Encodes SEQ ID NO: 20 I+ region, is codon optimized for yeast expression, and encodes a methionine initiation codon

&lt;400&gt; 51

```

atggctgaag aaactgggtg taccaacact gaagctcaac caaagaccga agctgtcgct 60
tccccaacca ctacctctga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 120
gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggct gtcaagccag ctactaaggc tgacaacaac 240

```

```

acttacccaa ttttgaacca agaattgaga gaagctatta agaaccacgc tatcaaggac 300
aaggaccact cgcgtccaaa ctctagacca atcgacttcg aaatgaagaa ggaaaacggt 360
gaacaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccgggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatataag ttgggttccct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tgggaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggt 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtagaag 1020
tacatggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080
agagtcagaa ccattctcaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1200
gacggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccattctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgctcttc tgaatccggt 1440
aagtaa
1446

```

&lt;210&gt; 52

&lt;211&gt; 1341

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Encodes the SEQ ID NO: 20 I region, is codon optimized for yeast expression, and encodes a methionine initiation codon

&lt;400&gt; 52

```

atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60
tccccaaaca ctacctctga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 120
gttttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggct gtcaagccag ctactaaggc tgacaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccacgc tatcaaggac 300
aaggaccact cgcgtccaaa ctctagacca atcgacttcg aaatgaagaa ggaaaacggt 360
gaacaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccgggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatataag ttgggttccct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tgggaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggt 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtagaag 1020
tacatggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080
agagtcagaa ccattctcaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1200
gacggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320

```

ccatctaagc caaccccata a

1341

&lt;210&gt; 53

&lt;211&gt; 1938

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Encodes for full length ORF0657n containing SEQ ID  
 NO: 20 modified to contain a glycine after the  
 amino terminus methionine and is codon optimized  
 for yeast expression

&lt;400&gt; 53

```

atgggtaaca agcaacaaaa ggaattcaag tctttctact ccattagaaa gtcttccttg 60
ggtgttgctt ctgtcgctat ctccaccttg ttgttggtga tgtctaacgg tgaagctcaa 120
gctgctgaag aaactgggtg taccaacact gaagctcaac caaagaccga agctgtcgct 180
tccccaacca ctacctctga aaagggtcca gaaactaagc cagttgctaa cgctgtctcc 240
gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 300
gaagtcaagg ctccaaagga aactaaggct gtcaagccag ctactaaggc tgacaacaac 360
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 420
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa ggaaaacggc 480
gaacaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 540
tctaagccag aaatcgaatt gggtttgcaa tccgggtcaat tctggagaaa gttcgaagtc 600
tacgaagggtg acaagaagtt gccaatgaag ttgggttctc acgacaccgt caaggactac 660
gcttacatca gattctccgt ttctaacggc actaaggctg tcaagattgt ctcttccacc 720
cacttcaaca acaaggaaga aaagtacgac tacactttga tggaattcgc tcaaccaatt 780
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggtc 840
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 900
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaaggct 960
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 1020
aagatgactg acttgcaaga cactaagtag gtcgtctacg aatccgctcg aaacaacgaa 1080
tccatgatgg acaccttcgt taagcaccca attagactg gtatgttgaa cggtagaag 1140
tacatgggtca tggaaacccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1200
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatat 1260
gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1320
gacggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1380
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1440
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1500
gacgacaaca agcaattgcc atccgtcgaa aagggaaaacg acgctccttc tgaatccggt 1560
aaggacaaga ctccagctac caagccagct aagggtgaag ttgaatcttc ctctactact 1620
ccaaccaagg ttgtctccac taccctaaac gtcgctaagc caactaccgc ttcttccaag 1680
actaccaagg acgttgtcca aacttctgct gggtcctctg aagctaagga ctctgctcca 1740
ttgcaaaagg ctaacatcaa gaacaccaac gacggtcaca cccaatccca aaacaacaag 1800
aacactcaag aaaacaaggc taagtctttg ccacaaaccg gtgaagaatc caacaaggac 1860
atgaccttgc cattgatggc tttgttggtc ttgtcttcca tcgttgcttt cgtcttgcca 1920
agaagagaa agaactaa
1938

```

&lt;210&gt; 54

&lt;211&gt; 565

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 54

Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu  
 1 5 10 15  
 Ala Val Ala Ser Pro Thr Thr Thr Thr Glu Lys Ala Pro Glu Ala Lys  
 20 25 30  
 Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro  
 35 40 45  
 Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Ala Pro Lys Glu Thr  
 50 55 60  
 Lys Ala Val Lys Pro Ala Ala Lys Ala Asp Asn Asn Thr Tyr Pro Ile  
 65 70 75 80  
 Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp  
 85 90 95  
 Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys  
 100 105 110  
 Lys Glu Asn Gly Glu Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys  
 115 120 125  
 Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly  
 130 135 140  
 Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp  
 145 150 155 160  
 Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr  
 165 170 175  
 Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile  
 180 185 190  
 Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr  
 195 200 205  
 Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys  
 210 215 220  
 Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys  
 225 230 235 240  
 Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp  
 245 250 255  
 Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Asp  
 260 265 270  
 Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe  
 275 280 285  
 Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr  
 290 295 300  
 Lys Tyr Ala Val Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp  
 305 310 315 320  
 Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys  
 325 330 335  
 Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met  
 340 345 350  
 Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn  
 355 360 365  
 Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp  
 370 375 380  
 Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr  
 385 390 395 400  
 His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp  
 405 410 415

Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala  
                   420                  425                  430  
 Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu  
                   435                  440                  445  
 Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser  
                   450                  455                  460  
 Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr  
 465                  470                  475                  480  
 Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser Ser Thr Thr  
                   485                  490                  495  
 Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr  
                   500                  505                  510  
 Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser Ala Ser Ser  
                   515                  520                  525  
 Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn  
                   530                  535                  540  
 Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu  
 545                  550                  555                  560  
 Asn Lys Ala Lys Ser  
                   565

&lt;210&gt; 55

&lt;211&gt; 568

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 55

Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu  
 1                  5                  10                  15  
 Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys  
                   20                  25                  30  
 Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro  
                   35                  40                  45  
 Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro  
                   50                  55                  60  
 Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr  
 65                  70                  75                  80  
 Tyr Pro Ile Leu Asn Gln Gly Leu Arg Glu Ala Ile Lys Asn Pro Ala  
                   85                  90                  95  
 Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe  
                   100                  105                  110  
 Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser  
                   115                  120                  125  
 Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile  
                   130                  135                  140  
 Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr  
 145                  150                  155                  160  
 Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val  
                   165                  170                  175  
 Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala  
                   180                  185                  190



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Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr
    195                200                205
Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp
    210                215                220
Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro
    225                230                235                240
Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys
    245                250                255
Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys
    260                265                270
Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Pro Ala Ile
    275                280                285
Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu
    290                295                300
Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser
    305                310                315                320
Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn
    325                330                335
Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys
    340                345                350
Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala
    355                360                365
Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr
    370                375                380
Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp
    385                390                395                400
Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala
    405                410                415
Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys
    420                425                430
Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val
    435                440                445
Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln
    450                455                460
Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys
    465                470                475                480
Asp Lys Thr Pro Ala Thr Lys Pro Thr Lys Gly Glu Val Glu Ser Ser
    485                490                495
Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys
    500                505                510
Pro Ile Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser
    515                520                525
Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn
    530                535                540
Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn
    545                550                555                560
Thr Gln Glu Asn Lys Ala Lys Ser
    565

```

&lt;210&gt; 56

&lt;211&gt; 568

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 56

Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu  
 1 5 10 15  
 Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys  
 20 25 30  
 Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro  
 35 40 45  
 Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro  
 50 55 60  
 Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr  
 65 70 75 80  
 Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Glu  
 85 90 95  
 Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe  
 100 105 110  
 Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser  
 115 120 125  
 Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile  
 130 135 140  
 Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr  
 145 150 155 160  
 Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val  
 165 170 175  
 Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Ile Ser Asn Gly Thr Lys Ala  
 180 185 190  
 Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr  
 195 200 205  
 Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp  
 210 215 220  
 Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro  
 225 230 235 240  
 Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys  
 245 250 255  
 Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys  
 260 265 270  
 Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile  
 275 280 285  
 Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu  
 290 295 300  
 Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser  
 305 310 315 320  
 Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn  
 325 330 335  
 Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys  
 340 345 350  
 Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala  
 355 360 365  
 Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr  
 370 375 380  
 Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp  
 385 390 395 400  
 Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala  
 405 410 415

```

Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys
      420      425      430
Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val
      435      440      445
Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln
      450      455      460
Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys
465      470      475      480
Asp Lys Thr Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser
      485      490      495
Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Val Lys
      500      505      510
Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser
      515      520      525
Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn
      530      535      540
Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn
545      550      555      560
Thr Gln Glu Asn Lys Ala Lys Ser
      565

```

&lt;210&gt; 57

&lt;211&gt; 568

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;221&gt; SITE

&lt;222&gt; 247

&lt;223&gt; Unknown

&lt;400&gt; 57

```

Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
  1      5      10      15
Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys
      20      25      30
Pro Val Ala Asn Ala Val Pro Val Ser Asn Lys Glu Val Glu Ala Pro
      35      40      45
Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro
      50      55      60
Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr
65      70      75      80
Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Thr Lys Asn Pro Glu
      85      90      95
Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Thr Asp Phe
      100      105      110
Glu Met Lys Lys Asn Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser
      115      120      125
Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile
      130      135      140
Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr
145      150      155      160

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Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val  
 165 170 175  
 Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Ile Ser Asn Gly Thr Lys Ala  
 180 185 190  
 Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr  
 195 200 205  
 Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp  
 210 215 220  
 Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro  
 225 230 235 240  
 Tyr Lys Lys Ala Lys Thr Xaa Glu Arg Gln Val Tyr Glu Leu Asn Lys  
 245 250 255  
 Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys  
 260 265 270  
 Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile  
 275 280 285  
 Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu  
 290 295 300  
 Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser  
 305 310 315 320  
 Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn  
 325 330 335  
 Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys  
 340 345 350  
 Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala  
 355 360 365  
 Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr  
 370 375 380  
 Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp  
 385 390 395 400  
 Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala  
 405 410 415  
 Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys  
 420 425 430  
 Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val  
 435 440 445  
 Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln  
 450 455 460  
 Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys  
 465 470 475 480  
 Asp Lys Thr Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser  
 485 490 495  
 Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys  
 500 505 510  
 Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser  
 515 520 525  
 Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn  
 530 535 540  
 Leu Leu Lys Thr His Asp Gly His Thr Gln Ser Gln Asn Ile Lys Asn  
 545 550 555 560  
 Thr Lys Lys Asp Lys Ala Lys Ser  
 565

&lt;210&gt; 58

&lt;211&gt; 568

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 58

```

Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
 1           5           10           15
Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys
          20           25           30
Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro
          35           40           45
Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro
          50           55           60
Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr
65           70           75           80
Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala
          85           90           95
Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe
          100          105          110
Glu Met Lys Lys Glu Asn Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser
          115          120          125
Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile
          130          135          140
Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr
145          150          155          160
Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val
          165          170          175
Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala
          180          185          190
Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr
          195          200          205
Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp
          210          215          220
Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro
225          230          235          240
Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys
          245          250          255
Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys
          260          265          270
Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile
          275          280          285
Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu
          290          295          300
Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser
305          310          315          320
Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn
          325          330          335
Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys
          340          345          350
Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala
          355          360          365
Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr
          370          375          380

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Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp  
 385 390 395 400  
 Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala  
 405 410 415  
 Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys  
 420 425 430  
 Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val  
 435 440 445  
 Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln  
 450 455 460  
 Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys  
 465 470 475 480  
 Asp Lys Thr Pro Ala Thr Lys Pro Thr Lys Gly Glu Val Glu Ser Ser  
 485 490 495  
 Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys  
 500 505 510  
 Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser  
 515 520 525  
 Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn  
 530 535 540  
 Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn  
 545 550 555 560  
 Thr Gln Glu Asn Lys Ala Lys Ser  
 565

&lt;210&gt; 59

&lt;211&gt; 567

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 59

Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu  
 1 5 10 15  
 Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys  
 20 25 30  
 Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro  
 35 40 45  
 Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro  
 50 55 60  
 Lys Glu Thr Lys Ala Val Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr  
 65 70 75 80  
 Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala  
 85 90 95  
 Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe  
 100 105 110  
 Glu Met Asn Lys Lys Asn Gly Glu Gln Gln Phe Tyr His Tyr Ala Ser  
 115 120 125  
 Ser Ala Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile  
 130 135 140  
 Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr  
 145 150 155 160

Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val  
 165 170 175  
 Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala  
 180 185 190  
 Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Asp  
 195 200 205  
 Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys  
 210 215 220  
 Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr  
 225 230 235 240  
 Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys Ile  
 245 250 255  
 Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu  
 260 265 270  
 Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile Thr  
 275 280 285  
 Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu Gln  
 290 295 300  
 Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser Met  
 305 310 315 320  
 Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn Gly  
 325 330 335  
 Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp  
 340 345 350  
 Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala Lys  
 355 360 365  
 Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr Leu  
 370 375 380  
 Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp Gly  
 385 390 395 400  
 Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala Asn  
 405 410 415  
 Thr Asp Lys Ser Asn Lys Lys Glu Gln Asp Asn Ser Ala Lys Lys  
 420 425 430  
 Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val Glu  
 435 440 445  
 Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu  
 450 455 460  
 Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp  
 465 470 475 480  
 Lys Thr Pro Ala Thr Lys Pro Thr Lys Gly Glu Val Glu Ser Ser Ser  
 485 490 495  
 Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys Pro  
 500 505 510  
 Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser Ala  
 515 520 525  
 Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile  
 530 535 540  
 Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn Thr  
 545 550 555 560  
 Gln Glu Asn Lys Ala Lys Ser  
 565

&lt;210&gt; 60

&lt;211&gt; 576

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 60

```

Ala Glu Glu Thr Gly Val Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
 1           5           10           15
Ala Val Ala Ser Pro Thr Thr Thr Thr Thr Glu Lys Ala Pro Glu Ala
          20           25           30
Lys Pro Val Ala Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys
          35           40           45
Glu Val Val Ala Pro Thr Thr Glu Thr Lys Glu Ala Lys Glu Val Lys
 50           55           60
Ala Val Lys Glu Val Lys Ala Pro Lys Glu Ala Lys Glu Glu Lys Pro
65           70           75           80
Ala Ala Lys Ala Asp Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu
          85           90           95
Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser Ala
          100          105          110
Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Lys Asp Gly Thr
          115          120          125
Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys Pro Ala Arg Val Ile
          130          135          140
Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly Gln
145          150          155          160
Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro Ile
          165          170          175
Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr Ala Tyr Ile Arg Phe
          180          185          190
Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile Val Ser Ser Thr His
          195          200          205
Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu Phe Ala
          210          215          220
Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp Tyr
225          230          235          240
Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu Glu
          245          250          255
Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp Lys Leu Pro Glu Lys
          260          265          270
Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Glu Thr Lys Lys Ala Leu
          275          280          285
Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln Pro
          290          295          300
Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Ala Tyr
305          310          315          320
Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp Thr Phe Val Lys His
          325          330          335
Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met Glu
          340          345          350
Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln Arg
          355          360          365
Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile Ile
          370          375          380

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Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys Val
385          390          395          400
His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile Val
          405          410          415
Asp Lys Glu Ala Phe Thr Lys Ala Asn Ala Asp Lys Thr Asn Lys Lys
          420          425          430
Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Thr Thr Pro Ala Met Pro
          435          440          445
Ser Lys Pro Thr Thr Pro Pro Val Glu Lys Glu Ser Gln Lys Gln Asp
          450          455          460
Ser Gln Lys Asp Asp Asn Lys Gln Ser Pro Ser Val Glu Lys Glu Asn
465          470          475          480
Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Met Pro Val Thr Lys Pro
          485          490          495
Ala Lys Ala Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val Val
          500          505          510
Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Glu Thr
          515          520          525
Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys Asp
          530          535          540
Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly His
545          550          555          560
Thr Gln Ser Gln Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys Ser
          565          570          575

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&lt;210&gt; 61

&lt;211&gt; 572

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 61

```

Ala Glu Glu Thr Gly Val Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
1          5          10          15
Ala Val Ala Ser Pro Thr Thr Thr Thr Thr Glu Lys Ala Pro Glu Ala
          20          25          30
Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Val Ala
          35          40          45
Pro Thr Thr Glu Thr Lys Glu Ala Lys Glu Val Lys Ala Val Lys Glu
          50          55          60
Val Lys Ala Pro Lys Glu Ala Lys Glu Glu Lys Pro Ala Ala Lys Ala
65          70          75          80
Asp Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile
          85          90          95
Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg
          100          105          110
Pro Ile Asp Phe Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr
          115          120          125
His Tyr Ala Ser Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser
          130          135          140
Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys
145          150          155          160

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Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser  
 165 170 175  
 Tyr Asp Thr Val Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn  
 180 185 190  
 Gly Thr Lys Ala Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys  
 195 200 205  
 Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr  
 210 215 220  
 Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys  
 225 230 235 240  
 Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr  
 245 250 255  
 Glu Leu Asn Lys Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu  
 260 265 270  
 Tyr Lys Lys Lys Leu Glu Glu Thr Lys Lys Ala Leu Asp Glu Gln Val  
 275 280 285  
 Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys  
 290 295 300  
 Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu  
 305 310 315 320  
 Asn Asn Glu Ser Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr  
 325 330 335  
 Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp  
 340 345 350  
 Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile  
 355 360 365  
 Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Cys Val  
 370 375 380  
 Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr  
 385 390 395 400  
 Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala  
 405 410 415  
 Phe Thr Lys Ala Asn Ala Asp Lys Thr Asn Lys Lys Glu Gln Gln Asp  
 420 425 430  
 Asn Ser Ala Lys Lys Glu Thr Thr Pro Ala Met Pro Ser Lys Pro Thr  
 435 440 445  
 Thr Pro Pro Val Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp  
 450 455 460  
 Asp Asn Lys Gln Ser Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser  
 465 470 475 480  
 Glu Ser Gly Lys Asp Lys Met Pro Val Thr Lys Pro Ala Lys Ala Glu  
 485 490 495  
 Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln  
 500 505 510  
 Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Glu Thr Thr Lys Asp Val  
 515 520 525  
 Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu  
 530 535 540  
 Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln  
 545 550 555 560  
 Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys Ser  
 565 570

&lt;210&gt; 62

&lt;211&gt; 572

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 62

Ala	Glu	Glu	Thr	Gly	Val	Thr	Asn	Thr	Glu	Ala	Gln	Pro	Lys	Thr	Glu	1	5	10	15
Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Thr	Thr	Glu	Lys	Ala	Pro	Glu	Ala	20	25	30	
Lys	Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Val	Ala	35	40	45	
Pro	Thr	Thr	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Ala	Val	Lys	Glu	50	55	60	
Val	Lys	Ala	Pro	Lys	Glu	Ala	Lys	Glu	Glu	Lys	Pro	Ala	Ala	Lys	Ala	65	70	75	80
Asp	Asn	Asn	Thr	Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	85	90	95	
Lys	Asn	Pro	Ala	Ile	Lys	Asp	Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	100	105	110	
Pro	Ile	Asp	Phe	Glu	Met	Lys	Lys	Lys	Asp	Gly	Thr	Gln	Gln	Phe	Tyr	115	120	125	
His	Tyr	Ala	Ser	Ser	Val	Lys	Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	130	135	140	
Lys	Pro	Glu	Ile	Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	145	150	155	160
Phe	Glu	Val	Tyr	Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	165	170	175	
Tyr	Asp	Thr	Val	Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	180	185	190	
Gly	Thr	Lys	Ala	Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	195	200	205	
Glu	Glu	Lys	Tyr	Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	210	215	220	
Asn	Ser	Ala	Asp	Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	225	230	235	240
Leu	Leu	Ala	Pro	Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	245	250	255	
Glu	Leu	Asn	Lys	Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	260	265	270	
Tyr	Lys	Lys	Lys	Leu	Glu	Glu	Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	275	280	285	
Lys	Ser	Ala	Ile	Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	290	295	300	
Met	Thr	Asp	Leu	Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	305	310	315	320
Asn	Asn	Glu	Ser	Met	Met	Asp	Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	325	330	335	
Gly	Met	Leu	Asn	Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	340	345	350	
Asp	Tyr	Trp	Lys	Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	355	360	365	
Ser	Lys	Asp	Ala	Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	370	375	380	

Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr  
 385 390 395 400  
 Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala  
 405 410 415  
 Phe Thr Lys Ala Asn Ala Asp Lys Thr Asn Lys Lys Glu Gln Gln Asp  
 420 425 430  
 Asn Ser Ala Lys Lys Glu Thr Thr Pro Ala Met Pro Ser Lys Pro Thr  
 435 440 445  
 Thr Pro Pro Val Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp  
 450 455 460  
 Asp Asn Lys Gln Ser Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser  
 465 470 475 480  
 Glu Ser Gly Lys Asp Lys Met Pro Val Thr Lys Pro Ala Lys Ala Glu  
 485 490 495  
 Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln  
 500 505 510  
 Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Glu Thr Thr Lys Asp Val  
 515 520 525  
 Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu  
 530 535 540  
 Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln  
 545 550 555 560  
 Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys Ser  
 565 570

&lt;210&gt; 63

&lt;211&gt; 566

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657nH

&lt;400&gt; 63

Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu  
 1 5 10 15  
 Ala Val Ala Ser Pro Thr Thr Thr Thr Thr Glu Lys Ala Pro Glu Ala  
 20 25 30  
 Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Val Ala  
 35 40 45  
 Pro Thr Thr Glu Thr Lys Glu Ala Lys Glu Val Lys Ala Pro Lys Glu  
 50 55 60  
 Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Asp Asn Asn Thr Tyr Pro  
 65 70 75 80  
 Ile Leu Asn Lys Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys  
 85 90 95  
 Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe Glu Met  
 100 105 110  
 Lys Lys Glu Asn Gly Glu Gln Gln Phe Tyr His Tyr Ala Ser Ser Val  
 115 120 125  
 Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu  
 130 135 140  
 Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly  
 145 150 155 160

Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val Lys Asp  
 165 170 175  
 Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala Val Lys  
 180 185 190  
 Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr  
 195 200 205  
 Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe  
 210 215 220  
 Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys  
 225 230 235 240  
 Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln  
 245 250 255  
 Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu  
 260 265 270  
 Glu Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile Thr Glu  
 275 280 285  
 Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp  
 290 295 300  
 Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Met  
 305 310 315 320  
 Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys  
 325 330 335  
 Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe  
 340 345 350  
 Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn  
 355 360 365  
 Asn Thr Arg Thr Ile Ile Phe Pro Tyr Ile Glu Gly Lys Thr Leu Tyr  
 370 375 380  
 Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln  
 385 390 395 400  
 Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Ala  
 405 410 415  
 Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu  
 420 425 430  
 Thr Thr Pro Ala Thr Pro Ser Lys Pro Thr Thr Pro Pro Val Glu Lys  
 435 440 445  
 Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Thr Gln Ser Pro  
 450 455 460  
 Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys  
 465 470 475 480  
 Thr Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser Ser Thr  
 485 490 495  
 Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr  
 500 505 510  
 Thr Ala Ser Ser Glu Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly  
 515 520 525  
 Pro Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys  
 530 535 540  
 Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln  
 545 550 555 560  
 Glu Asp Lys Ala Lys Ser  
 565

&lt;210&gt; 64

&lt;211&gt; 8

<212> PRT  
<213> Artificial Sequence

<220>  
<223> His-Tag

<400> 64  
Leu Glu His His His His His His  
1 5

<210> 65  
<211> 16  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 65  
ctggccgtcg ttttac 16

<210> 66  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 66  
caggaaacag ctatgac 17

<210> 67  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 67  
aaccggtttt ccatggggaa caaacagcaa aaagaattt 39

<210> 68  
<211> 38  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 68  
accggtttct cgagggtttt acgttttcta ggtaatac 38

<210> 69

<211> 109  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> ORF0657n oligomer

<400> 69  
atgggtaaca agcaacaaaa ggaattcaag tctttctact ccattagaaa gtcttccttg 60  
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&lt;210&gt; 74

&lt;211&gt; 109

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657n oligomer

&lt;400&gt; 74

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&lt;210&gt; 75

&lt;211&gt; 102

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657n oligomer

&lt;400&gt; 75

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&lt;210&gt; 76

&lt;211&gt; 104

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657n oligomer

&lt;400&gt; 76

ctgatgtaag cgtagtcctt gacgggtgtcg taggaaacca acttaattgg caacttcttg 60  
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&lt;210&gt; 77

&lt;211&gt; 109

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657n oligomer

&lt;400&gt; 77

caccgtcaag gactacgctt acatcagatt ctccgtttct aacggtacta aggctgtcaa 60  
gattgtctct tccacccact tcaacaacaa ggaagaaaag tacgactac 109

&lt;210&gt; 78

&lt;211&gt; 109

&lt;212&gt; DNA



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&lt;400&gt; 87

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cccaaaagga cgacaacaag caatt 85

&lt;210&gt; 88

&lt;211&gt; 100

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657n oligomer

&lt;400&gt; 88

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&lt;210&gt; 89

&lt;211&gt; 101

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657n oligomer

&lt;400&gt; 89

ggacaagact ccagctacca agccaactaa ggggtgaagtt gaatcttcct ctactactcc 60  
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&lt;210&gt; 90

&lt;211&gt; 101

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&lt;213&gt; Artificial Sequence

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&lt;223&gt; ORF0657n oligomer

&lt;400&gt; 90

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&lt;210&gt; 91

&lt;211&gt; 91

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ORF0657n oligomer

&lt;400&gt; 91

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<213> Artificial Sequence

<220>

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<400> 98

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<211> 42

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<223> Primer

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<400> 105  
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38

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<213> S. aureus

&lt;400&gt; 106

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Met Ser Asn Gly Glu Ala Gln Ala Glu Glu Thr Gly Gly Thr Asn
          35          40          45
Thr Glu Ala Gln Pro Lys Thr Glu Ala Leu Ala Ser Pro Thr Thr Thr
          50          55          60
Thr Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser Val
65          70          75          80
Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala Lys
          85          90          95
Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Ala Val Lys Pro
          100          105          110
Ala Ala Lys Ala Asp Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu
          115          120          125
Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser Ala
          130          135          140
Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Glu Asn Gly Glu
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Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys Pro Ala Arg Val Ile
          165          170          175
Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly Gln
          180          185          190
Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro Ile
          195          200          205
Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr Ala Tyr Ile Arg Phe
          210          215          220
Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile Val Ser Ser Thr His
          225          230          235          240
Phe Asn Asn Lys Glu Lys Tyr Asp Tyr Thr Leu Met Glu Phe Ala
          245          250          255
Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp Tyr
          260          265          270
Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu Glu
          275          280          285
Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp Lys Leu Pro Glu Lys
          290          295          300
Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Asp Thr Lys Lys Ala Leu
          305          310          315          320
Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln Pro
          325          330          335
Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Val Tyr
          340          345          350
Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp Thr Phe Val Lys His
          355          360          365
Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met Glu
          370          375          380
Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln Arg
          385          390          395          400
Val Arg Thr Ile Ser Lys Asp Ala Ile Asn Asn Thr Arg Thr Ile Ile
          405          410          415
Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys Val
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His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile Val  
 435 440 445  
 Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp Lys Ser Asn Lys Lys  
 450 455 460  
 Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala Thr Pro Ala Thr Pro  
 465 470 475 480  
 Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys Gln Asp  
 485 490 495  
 Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys Glu Asn  
 500 505 510  
 Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys Pro  
 515 520 525  
 Ala Lys Gly Glu Val Glu Ser Ser Thr Thr Pro Thr Lys Val Val  
 530 535 540  
 Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Lys Thr  
 545 550 555 560  
 Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys Asp  
 565 570 575  
 Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly His  
 580 585 590  
 Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys Ser  
 595 600 605  
 Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu Pro Leu  
 610 615 620  
 Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu Pro Arg  
 625 630 635 640  
 Lys Arg Lys Asn

&lt;210&gt; 107

&lt;211&gt; 644

&lt;212&gt; PRT

&lt;213&gt; S. aureus

&lt;400&gt; 107

Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys  
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 Met Ser Asn Gly Glu Ala Gln Ala Ala Glu Glu Thr Gly Gly Thr Asn  
 35 40 45  
 Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr Thr  
 50 55 60  
 Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser Val  
 65 70 75 80  
 Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala Lys  
 85 90 95  
 Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Ala Val Lys Pro  
 100 105 110  
 Ala Thr Lys Ala Asp Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu  
 115 120 125  
 Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser Ala  
 130 135 140  
 Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Glu Asn Gly Glu  
 145 150 155 160



Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser	Ser	Val	Lys	Pro	Ala	Arg	Val	Ile		
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Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile	Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln		
			180					185					190				
Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr	Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile		
		195					200					205					
Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val	Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe		
	210					215					220						
Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	Val	Lys	Ile	Val	Ser	Ser	Thr	His		
225					230					235					240		
Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala		
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Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr		
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Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu		
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Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	Gly	Lys	Lys	Tyr	Met	Val	Met	Glu		
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His	Val	Lys	Thr	Ile	Asp	Tyr	Asp	Gly	Gln	Tyr	His	Val	Arg	Ile	Val		
	435					440					445						
Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala	Asn	Thr	Asp	Lys	Ser	Asn	Lys	Lys		
	450					455					460						
Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys	Lys	Glu	Ala	Thr	Pro	Ala	Thr	Pro		
465					470					475					480		
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Ser	Gln	Lys	Asp	Asp	Asn	Lys	Gln	Leu	Pro	Ser	Val	Glu	Lys	Glu	Asn		
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Ala	Lys	Gly	Glu	Val	Glu	Ser	Ser	Ser	Thr	Thr	Pro	Thr	Lys	Val	Val		
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Ser	Thr	Thr	Gln	Asn	Val	Ala	Lys	Pro	Thr	Thr	Ala	Ser	Ser	Lys	Thr		
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Thr	Gln	Ser	Gln	Asn	Asn	Lys	Asn	Thr	Gln	Glu	Asn	Lys	Ala	Lys	Ser
		595					600					605			
Leu	Pro	Gln	Thr	Gly	Glu	Glu	Ser	Asn	Lys	Asp	Met	Thr	Leu	Pro	Leu
	610					615					620				
Met	Ala	Leu	Leu	Ala	Leu	Ser	Ser	Ile	Val	Ala	Phe	Val	Leu	Pro	Arg
625					630					635					640
Lys	Arg	Lys	Asn												